

GTTTAGTCTGCAGCCGAGCAGCTAAAGGAGAGAAATCGCTCAGGAAAGACACACTGCAGACTCCACCGCACCCCTGC										79
AATAGATGGTTCCGACTACACAAGGAGAGAAACCGGAGGTGACACTCTCCTGCCTGGAAGAGGACGAAACGACCCAAA										158
CAAACGCAAGGACTGGACTCCATGCCGAAAGGTATCTGGAAGTCGTGACACACGGTGTGTATAAACAACAAAGTTTGGCGAGCT										237
GTTAATTGCTGTGCTGTATTAAAGAGACGCTTTCAAGTTTCAAGTACCAAAATGTAGCTTTACGTTGCCAAAGGAAGT										316
TGAGGCAATTGCTTTGCTGTTTTAACTTGCTCTGTGAGGAAATCTCATAAACTGACCA										
M H Q M N										5
ATG CAC CAA ATG AAT										390
A K M H F R F V F A L L I V S F N H D V										25
GCT AAA ATG CAC TTT AGG TTT GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA										450
L G K N L K Y R I Y E E Q R V G S V I A										45
CTG GGC AAG AAT TTG AAA TAC AGG ATT TAT GAG GAA CAG AGG GTT GGA TCA GTA ATT GCA										510
R L S E D V A D V L L L K L P N P S T V R										65
AGA CTA TCA GAG GAT GTG GCT GAT GTT TTA TTG AAG CTT CCT AAT CCT TCT ACT GTT CGA										570
F R A M Q R G N S P L L L V V N E D N G E										85
TTT CGA GCC ATG CAG AGG GGA AAT TCT CCT CTA CTT GTA GTA AAC GAG GAT AAT GGG GAA										630

Fig. 1A

I	S	I	G	A	T	I	D	R	E	Q	L	C	Q	K	N	L	N	C	S	105
ATC	AGC	ATA	GGG	GCT	ACA	ATT	GAC	CGT	GAA	CAA	CTG	TGC	CAG	AAA	AAC	TTG	AAC	TGT	TCC	690
I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	2/361 930
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110

Fig. 1B

F E Q Q S Y I I Q L L E N S P V G T L L 265
 TTT GAG CAG CAA TCT TAT ATA ATA CAA CTC TTA GAA AAC TCC CCG GTT GGC ACT TTG CTC 1170

L D L N A T D P D E G A N G K I V Y S F 285
 TTA GAT CTG AAT GCC ACG GAT CCA GAT GAG GGC GCT AAT GGG AAA ATT GTA TAT TCC TTC 1230

S S H V S P K I M E T F K I D S E R G H 305
 AGC AGT CAT GTG TCT CCC AAA ATT ATG GAG ACT TTT AAA ATT GAT TCT GAA AGA GGA CAT 1290

L T L F K Q V D Y E I T K S Y E I D V Q 325
 TTG ACT CTT TTC AAG CAA GTG GAT TAT GAA ATC ACC AAA TCC TAT GAG ATT GAT GTT CAG 1350

A Q D L G P N S I P A H C K I I I K V V 345
 GCT CAA GAT TTG GGT CCA AAT TCA ATC CCA GCC CAT TGC AAA ATT ATA ATT AAG GTT GTG 1410

D V N D N K P E I N I N L M S P G K E E 365
 GAT GTT AAT GAC AAT AAA CCT GAA ATT AAC ATC AAC CTC ATG TCC CCT GGA AAA GAA GAA 1470

I S Y I F E G D P I D T F V A L V R V Q 385
 ATA TCT TAT ATT TTT GAA GGG GAT CCT ATT GAT ACA TTT GTT GCT TTG GTC AGA GTT CAG 1530

D K D S G L N G E I V C K L H G H G H F 405
 GAC AAG GAT TCT GGG CTG AAT GGA GAA ATA GTT TGT AAG CTT CAT GGA CAT GGT CAC TTT 1590

Fig. 1C

K L Q K T Y E N N Y L I L T N A T L D R 425
 AAA CTT CAG AAG ACA TAT GAA AAC AAT TAT TTA ATC TTA ACT AAT GCC ACA CTG GAT AGA 1650

 E K R S E Y S L T V I A E D R G T P S L 445
 GAA AAG AGA TCT GAG TAT AGT TTG ACT GTA ATC GCT GAG GAC AGG GGG ACA CCC AGT CTC 1710

 S T V K H F T V Q I N D I N D N P P H F 465
 TCT ACA GTG AAA CAT TTT ACA GTT CAA ATC AAT GAT ATC AAT GAC AAT CCA CCC CAC TTC 1770

 Q R S R Y E F V I S E N N S P G A Y I T 485
 CAG AGA AGC CGA TAT GAA TTT GTA ATT TCA GAA AAT AAC TCA CCA GGG GCA TAT ATC ACC 1830

 T V T A T D P D L G E N G Q V T Y T I L 505
 ACT GTT ACA GCC ACA GAT CCT GAT CTT GGA GAA AAT GGG CAA GTG ACA TAC ACC ATC TTG 1890

 E S F I L G S S I T T Y V T I D P S N G 525
 GAG AGT TTT ATT CTA GGA AGT TCC ATA ACT ACA TAT GTA ACC ATT GAC CCA TCT AAT GGA 1950

 A I Y A L R I F D H E E V S Q I T F V V 545
 GCC ATC TAT GCC CTC AGA ATC TTT GAT CAT GAA GAA GTG AGT CAG ATC ACT ACT TTT GTG GTA 2010

 E A R D G G S P K Q L V S N T T V V L T 565
 GAA GCA AGA GAT GGA AGC AGC CCG AAG CAA CTG GTA AGC AAT ACC ACA GTT GTG CTC ACC 2070

Fig. 1D

I I D E N D N V P V V I G P A L R N N T 585
ATC ATT GAC GAA AAT GAC AAC GTT CCT GTG GTT ATA GGG CCT GCA TTG CGT AAT AAT ACG 2130

A E I T I P K G A E S G F H V T R I R A 605
GCA GAA ATC ACC ATT CCC AAA GGG GCT GAA AGT GGC TTT CAT GTC ACA AGA ATA AGG GCA 2190

I D R D S G V N A E L S C A I V A G N E 625
ATT GAC AGA GAC TCT GGT GTG AAT GCT GAA CTC AGC TGC GCC ATA GTA GCA GGT AAT GAG 2250

E N I F I I D P R S C D I H T N V S M D 645
GAG AAT ATC TTC ATA ATT GAT CCA CGA TCA TGT GAC ATC CAT ACC AAC GTT AGC ATG GAT 2310

S V P Y T E W E L S V I I Q D K G N P Q 665
TCT GTT CCC TAC ACA GAA TGG GAG CTG TCA GTT ATC ATT CAG GAC AAA GGC AAT CCT CAG 2370

L H T K V L L K C M I F E Y A E S V T S 685
CTA CAT ACC AAA GTC CTT CTG AAG TGC ATG ATC TTT GAA TAT GCA GAG TCG GTG ACA AGT 2430

T A M T S V S Q A S L D V S M I I I I S 705
ACA GCA ATG ACT TCA GTA AGC CAG GCA TCC TTG GAT GTC TCC ATG ATA ATA ATT ATT TCC 2490

L G A I C A V L L V I M V L F A T R C N 725
TTA GGA GCA ATT TGT GCA GTG TTG CTG GTT ATT ATG GTG CTA TTT GCA ACT AGG TGT AAC 2550

Fig. 1E

R	E	K	K	D	T	R	S	Y	N	C	R	V	A	E	S	T	Y	Q	H	745
CGC	GAG	AAG	AAA	GAC	ACT	AGA	TCC	TAT	AAC	TGC	AGG	GTG	GCC	GAA	TCA	ACT	TAC	CAG	CAC	2610
H	P	K	R	P	S	R	Q	I	H	K	G	D	I	T	L	V	P	T	I	765
CAC	CCA	AAA	AGG	CCA	TCC	CGG	CAG	ATT	CAC	AAA	GGG	GAC	ATC	ACA	TTG	GTG	CCT	ACC	ATA	2670
N	G	T	L	P	I	R	S	H	H	R	S	S	P	S	S	S	P	T	L	785
AAT	GGC	ACT	CTG	CCC	ATC	AGA	TCT	CAT	CAC	AGA	TGG	TCT	CCA	TCT	TCA	TCT	CCT	ACC	TTA	2730
E	R	G	Q	M	G	S	R	Q	S	H	N	S	H	Q	S	L	N	S	L	805
GAA	AGA	GGG	CAG	ATG	GGC	AGC	CGG	CAG	AGT	CAC	AAC	AGT	CAC	CAG	TCA	CTC	AAC	AGT	TTG	2790
V	T	I	S	S	N	H	V	P	E	N	F	S	L	E	L	T	H	A	T	825
GTG	ACA	ATC	TCA	TCA	AAC	CAC	GTG	CCA	GAG	AAT	TTC	TCA	TTA	GAA	CTC	ACC	CAC	GCC	ACT	2850
P	A	V	E	Q	V	S	Q	L	L	S	M	L	H	Q	G	Q	Y	Q	P	845
CCT	GCT	GTT	GAG	CAG	GTC	TCT	CAG	CTT	CTT	TCA	ATG	CTT	CAC	CAG	GGG	CAA	TAT	CAG	CCA	2910
R	P	S	F	R	G	N	K	Y	S	R	S	Y	R	Y	A	L	Q	D	M	865
AGA	CCA	AGT	TTT	CGA	GGA	AAC	AAA	TAT	TCC	AGG	AGC	TAC	AGA	TAT	GCC	CTT	CAA	GAC	ATG	2970
D	K	F	S	L	K	D	S	G	R	G	D	S	E	A	G	D	S	D	Y	885
GAC	AAA	TTT	AGC	TTG	AAA	GAC	AGT	GGC	CGT	GGT	GAC	AGT	GAG	GCA	GGA	GAC	AGT	GAT	TAT	3030

Fig. 1F

D L G R D S P I D R L L G E G F S D L F 905
 GAT TTG GGG CGA GAT TCT CCA ATA GAT AGG CTG CTG GGT GAA GGA TTC AGC GAC CTG TTT 3090

 L T D G R I P A A M R L C T E E C R V L 925
 CTC ACA GAT GGA AGA ATT CCA GCA GCT ATG AGA CTC TGC ACG GAG GAG TGC AGG GTC CTG 3150

 G H S D Q C W M P P L P S P S D Y R S 945
 GGA CAC TCT GAC CAG TGC TGG ATG CCA CCA CTG CCC TCA CCG TCT TCT GAT TAT AGG AGT 3210

 N M F I P G E E F P T Q P Q Q H P H Q 965
 AAC ATG TTC ATT CCA GGG GAA GAA TTC CCA ACG CAA CCC CAG CAG CAG CAT CCA CAT CAG 3270

 S L E D D A Q P A D S G E K K K S F S T 985
 AGT CTT GAG GAT GAC GCT CAG CCT GCA GAT TCC GGT GAA AAG AAG AGT TTT TCC ACC 3330

 F G K D S P N D E D T G D T S T S L L 1005
 TTT GGA AAG GAC TCC CCA AAC GAT GAG GAC ACT GGG GAT ACC AGC ACA TCA TCT CTG CTC 3390

 S E M S S V F Q R L L P P S L D T Y S E 1025
 TCG GAA ATG AGC AGT GTG TTC CAG CGT CTC TTA CCG CCT TCC CTG GAC ACC TAT TCT GAA 3450

 C S E V D R S N S L E R R K G P L P A K 1045
 TGC AGT GAG GTG GAT CGG TCC AAC TCC CTG GAG CGC AGG AAG GGA CCC TTG CCA GCC AAA 3510

Fig. 1G

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AGACAAATGATGAAAAACAGAACTAAAGTCAATGTTTCCCTGACTCCCAGGCCCTACTATTCCAGGCCATCACACTGGCCT 4494
 GTTCCGGAGAAATATTCTCTCACAAATATATATCTACTTATAATTATGGTAAACAATAAAATTTTATTCCATCCTTGTA 4573
 GTATGAAACATGCTCCAAGGAAATGGAACTGTCTCTTAAATGGATAACAGTATGTGTTCTAATGGCATAAAAATATTAC 4652
 TGGATAAAAAACAGTTGTGTCAGTGTCTCTCCCTAAGGTAGTAAATATAATTGACTTATTCTGAACCCATTCTATTTTGAA 4731
 TCTCCCCCTTTCCCTCACAAATACCTTGAACATTTTAACTCTTTTGGAATATTGTCTTTCTTTGTTATAAATACTATTTT 4810
 AGCTTTTGTCTCCAGTGCAATGATCTCATATTTTGTCTTTTATTAGTATAAGAACATTTATAAAAAATCATATTTTGT 4889
 TACTGCAATTGTTTATTGTTGTGGCAAAATGAGAAATCCTTTATTATTGTGCTGTGATCTCTCTGTGGAAATGC 4968
 CTTGGTGAGAGAGATGCTTATTATGACTATTATCATTTCTGACCAAGCTTCTAATTAATGTTATTCTAATAATACACTA 5047
 TCTTGATTGTACTCTCCAGAAAAATTTTCTGTGAGTGAATAAAGAAAAATTAAGTAAAAAATAAAAAA 5121

Fig. 11

GTTTAGTCTGCAGCCGAGCAGCTAAAGGAGAAAGAAATCGCTCAGGAAAGACACACTGCAGACTCCACCGCACCCCTGC	79
AATAGATGGGTTCCGACTACACAAGGAGAGAAAACGGGAGGTGACACTCTCCTGCCCTGGAAAGAGGACGAAACGACCAAA	158
CAAACGCAAGGACTGGACTCCATGCCGAAAGTATCTGGAAGTCGTGACACGGTGTGTATAAAACAAAAGTTTGGCAGCT	237
GTTAAATTGCTGTGCTGTGTTATTAAAGAGACGCTTTCAAGTTTCAAGTACCAAAATGTAGCTTTACGTTGCCAAAAGGAAGT	316
TGAGGCAATTGCTTTTGCTGTGCTTTTAACTTGCTCTGTGAGGAAATCTCATAAACTGACCA ATG CAC CAA ATG AAT	5 390
A K M H F R F V F A L L I V S F N H D V	25
GCT AAA ATG CAC TTT AGG TTT GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA	450
L G K N L K Y R I Y E E Q R V G S V I A	45 510
CTG GGC AAG AAT TTG AAA TAC AGG ATT TAT GAG GAA CAG AGG GTT GGA TCA GTA ATT GCA	10/361 570
R L S E D V A D V L L L K L P N P S T V R	65
AGA CTA TCA GAG GAT GTG GCT GAT GTT TTA TTG AAG CTT CCT AAT CCT TCT ACT GTT CGA	570
F R A M Q R G N S P L L V V N E D N G E	85
TTT CGA GCC ATG CAG AGG GGA AAT TCT CCT CTA CTT GTA GTA AAC GAG GAT AAT GGG GAA	630
I S I G A T I D R E Q L C Q K N L N C S	105
ATC AGC ATA GGG GCT ACA ATT GAC CGT GAA CAA CTG TGC CAG AAA AAC TTG AAC TGT TCC	690

Fig. 2A

I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	930
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110
F	E	Q	Q	S	Y	I	I	Q	L	L	E	N	S	P	V	G	T	L	L	265
TTT	GAG	CAG	CAA	TCT	TAT	ATA	ATA	CAA	CTC	TTA	GAA	AAC	TCC	CCG	GTT	GGC	ACT	TTG	CTC	1170

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Fig. 2B

L D L N A T D P D E G A N G K I V Y S F 285
 TTA GAT CTG AAT GCC ACG GAT CCA GAT GAG GGC GCT AAT GGG AAA ATT GTA TAT TCC TTC 1230

 S S H V S P K I M E T F K I D S E R G H 305
 AGC AGT CAT GTG TCT CCC AAA ATT ATG GAG ACT TTT AAA ATT GAT TCT GAA AGA GGA CAT 1290

 L T L F K Q V D Y E I T K S Y E I D V Q 325
 TTG ACT CTT TTC AAG CAA GTG GAT TAT GAA ATC ACC AAA TCC TAT GAG ATT GAT GTT CAG 1350

 A Q D L G P N S I P A H C K I I K V V 345
 GCT CAA GAT TTG GGT CCA AAT TCA ATC CCA GCC CAT TGC AAA ATT ATA ATT AAG GTT GTG 1410

 D V N D N K P E I N I N L M S P G K E E 365
 GAT GTT AAT GAC AAT AAA CCT GAA ATT AAC ATC AAC CTC ATG TCC CCT GGA AAA GAA GAA 1470

 I S Y I F E G D P I D T F V A L V R V Q 385
 ATA TCT TAT ATT TTT GAA GGG GAT CCT ATT GAT ACA TTT GTT GCT TTG GTC AGA GTT CAG 1530

 D K D S G L N G E I V C K L H G H F 405
 GAC AAG GAT TCT GGG CTG AAT GGA GAA ATA GTT TGT AAG CTT CAT GGA CAT GGT CAC TTT 1590

 K L Q K T Y E N N Y L I L T N A T L D R 425
 AAA CTT CAG AAG ACA TAT GAA AAC AAT TAT TTA ATC TTA ACT AAT GCC ACA CTG GAT AGA 1650

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Fig. 2C

E	K	R	S	E	Y	S	L	T	V	I	A	E	D	R	G	T	P	S	L	445
GAA	AAG	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GGG	ACA	CCC	AGT	CTC	1710
S	T	V	K	H	F	T	V	Q	I	N	D	I	N	D	N	P	P	H	F	465
TCT	ACA	GTG	AAA	CAT	TTT	ACA	GTT	CAA	ATC	AAT	GAT	ATC	AAT	GAC	AAT	CCA	CCC	CAC	TTC	1770
Q	R	S	R	Y	E	F	V	I	S	E	N	N	S	P	G	A	Y	I	T	485
CAG	AGA	AGC	CGA	TAT	GAA	TTT	GTA	ATT	TCA	GAA	AAT	AAC	TCA	CCA	GGG	GCA	TAT	ATC	ACC	1830
T	V	T	A	T	D	P	D	L	G	E	N	G	Q	V	T	Y	T	I	L	505
ACT	GTT	ACA	GCC	ACA	GAT	CCT	GAT	CTT	GGA	GAA	AAT	GGG	CAA	GTG	ACA	TAC	ACC	ATC	TTG	1890
E	S	F	I	L	G	S	S	I	T	T	Y	V	T	I	D	P	S	N	G	525
GAG	AGT	TTT	ATT	CTA	GGA	AGT	TCC	ATA	ACT	ACA	TAT	GTA	ACC	ATT	GAC	CCA	TCT	AAT	GGA	1950
A	I	Y	A	L	R	I	F	D	H	E	E	V	S	Q	I	T	F	V	V	545
GCC	ATC	TAT	GCC	CTC	AGA	ATC	TTT	GAT	CAT	GAA	GAA	GTG	AGT	CAG	ATC	ACT	TTT	GTG	GTA	2010
E	A	R	D	G	G	S	P	K	Q	L	V	S	N	T	T	V	V	L	T	565
GAA	GCA	AGA	GAT	GGA	GGA	AGC	CCG	AAG	CAA	CTG	GTA	AGC	AAT	ACC	ACA	GTT	GTG	CTC	ACC	2070
I	I	D	E	N	D	N	V	P	V	V	I	G	P	A	L	R	N	N	T	585
ATC	ATT	GAC	GAA	AAT	GAC	AAC	GTT	CCT	GTG	GTT	ATA	GGG	CCT	GCA	TTG	CGT	AAT	AAT	ACG	2130

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Fig. 2D

Sequence

A E I T I P K G A E S G F H V T R I R A 605
 GCA GAA ATC ACC ATT CCC AAA GGG GCT GAA AGT GGC TTT CAT GTC ACA AGA ATA AGG GCA 2190

 I D R D S G V N A E L S C A I V A G N E 625
 ATT GAC AGA GAC TCT GGT GTG AAT GCT GAA CTC AGC TGC GCC ATA GTA GCA GGT AAT GAG 2250

 E N I F I I D P R S C D I H T N V S M D 645
 GAG AAT ATC TTC ATA ATT GAT CCA CGA TCA TGT GAC ATC CAT ACC AAC GTT AGC ATG GAT 2310

 S V P Y T E W E L S V I I Q D K G N P Q 665
 TCT GTT CCC TAC ACA GAA TGG GAG CTG TCA GTT ATC ATT CAG GAC AAA GGC AAT CCT CAG 2370

 L H T K V L L K C M I F E Y A E S V T S 685
 CTA CAT ACC AAA GTC CTT CTG AAG TGC ATG ATC TTT GAA TAT GCA GAG TCG GTG ACA AGT 2430

 T A M T S V S Q A S L D V S M I I I I S 705
 ACA GCA ATG ACT TCA GTA AGC CAG GCA TCC TTG GAT GTC TCC ATG ATA ATA ATT ATT TCC 2490

 L G A I C A V L L V I M V L F A T R C N 725
 TTA GGA GCA ATT TGT GCA GTG TTG CTG GTT ATT ATG GTG CTA TTT GCA ACT AGG TGT AAC 2550

 R E K K D T R S Y N C R V A E S T Y Q H 745
 CGC GAG AAG AAA GAC ACT AGA TCC TAT AAC TGC AGG GTG GCC GAA TCA ACT TAC CAG CAC 2610

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Fig. 2E

Fig. 2F

Fig. 2F

L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	924
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3147
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	944
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3207
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	964
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3267
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	984
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3327
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1004
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3387
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	L	D	T	Y	S	E	1024
TCG	GAA	ATG	AGC	AGT	GTG	TTC	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3447
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1044
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3507
T	V	G	Y	P	Q	G	V	A	A	W	A	A	S	T	H	F	Q	N	P	1064
ACT	GTG	GGT	TAC	CCA	CAG	GGG	GTA	GCG	GCA	TGG	GCA	GCC	AGT	ACG	CAT	TTT	CAA	AAT	CCC	3567

Fig. 2G

T N C G P P L G T H S S V Q P S S K W 1084
 ACC ACC AAC TGT GGT CCG CCA CTT GGA ACT CAC TCC AGT GTG CAG CCT TCT TCA AAA TGG 3627

 L P A M E E I P E N Y E D D F D N V L 1104
 CTG CCA GCC ATG GAG GAG ATC CCT GAA AAT TAT GAG GAA GAT GAT TTT GAC AAT GTG CTC 3687

 N H L N D G K H E L M D A S E L V A E I 1124
 AAC CAC CTC AAT GAT GGT AAA CAC GAA CTC ATG GAT GCC AGT GAA CTG GTG GCA GAG ATT 3747

 N K L L Q D V R Q S * 1134
 AAC AAA CTG CTT CAA GAT GTC CGC CAG AGC TAG 3780

 17/361
 GAGATTTAGCGAAGCATTTTGTTCATGTATATGGAATAGGGAACAACAACAACCAAAACCCCTGAAAGAAC 3859
 TGGCATTGCCAAATAGTTGCATTTATCATAAATGTCTGTATATGAATATTAATACTGTATTTTCGTATGTACA 3938
 CAATGCAAGTGTGATTATTTAAATCTGATTTTAAATAATACATTTGTACCTTATATTTATGTGTAATTTAAACAAACAAA 4017
 TTTTATTTTTTACTCCCATGACAGACATGTTTTTCCTAGTCGTGTAGAAAACCTAGCCACTGTTCAAATCTGATACACTA 4096
 TTCAACCAACAAGTAAAGCACTGCTTAGATTAGTTTGTGTTGGGAAGAATTATTTATGTTGTATGAACAAACCCCACT 4175
 GAAGCATTATACAAATCTTAATCCATTAAAGTGATCCCACTTTTTCATAAATCTTTTAGAAAATTAAGAATCATTA 4254
 ATTGTTAAGCTATTTTATTTATTTTCTACTTTCTACTAGCCCAATAGTTGAACCTTTATAGAAAATCGAAAGA 4333
 TAAAGTGAAAGTTTATTTCAAGGACTGAGAAATATCTTGAAGGTTATTTATAGATGACTATCTCAAATGAACCTTTTAT 4412
 AGACAATGATGAAACAGAACTAAAGTCAATGTTTCTGACTCCAGGCCCTACTATTCAGGCCATCACACTGGCCT 4491
 GTTCCGGAGAAATATTTCTCTCACAATATTAATCTACTTAAATATGTTAAACAATAAATTTTATTCATCCTTGTA 4570
 GTATGAAACATGCTCCAAGGAAATGGAATCTGTCTTTAAATGGAATAACAGTATGTGTTCTAATGGCATAAAATATAC 4649
 TGGATAAAAACAGTTGTGTGTCAGTGTCTCTCCTAAGGTAGTAAATATAATTGACTTATTTCTGAACCCCACTTCTATTGAA 4728

Fig. 2H

TCTCCCCTTCCCTCACAATACTTGAACATTTTAATCTTTTGGAAATATTGTCCTTTCTTTGTTATAACTATTTCATTTT 4807
 AGCTTTTGTCTCCAGTGCATGATCTCATATTTTGTCTTTTATTTTATTTTAGTATAAGAACATTTATATAAAATCATATTTTGT 4886
 TACTGCAATTGTTTATTTGTTGTGGCAAAATGAGAAATCCCTTTATTTATTTGTCTGTGATCTCTCTGTGTGGAATGC 4965
 CTTGGTGAGAGAGATGCTTATATGACTATATATCATTTCTGACCAAGCTTCTATTAATGTTATTCTAATAATACACTA 5044
 TCTTGATTGTACTCTCCAGAAAAATTTTCTGTCAGTGAAAAATAAGAAAAATTAAGTAAAAAATAAAAAA 5118

Fig. 2I

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T416      1651 GAAAAGAGATCTGAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGAC 1700
          |||||||
AL137471  1 ...AAGAGATCTGAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGAC 47

T416      1701 ACCCAGTCTCTCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA 1750
          |||||||
AL137471  48 ACCCAGTCTCTCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA 97

T416      1751 ATGACAAATCCACCCCACTTCCAGAGAAAGCCGATATGAATTTGTAAATTTC 1800
          |||||||
AL137471  98 ATGACAAATCCACCCCACTTCCAGAGAAAGCCGATATGAATTTGTAAATTTC 147

T416      1801 GAAAATAACTCACAGGGGCATATATCACCACTGTGTACAGCCACAGATCC 1850
          |||||||
AL137471  148 GAAAATAACTCACAGGGGCATATATCACCACTGTGTACAGCCACAGATCC 197

T416      1851 TGATCTTGGAGAAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTFA 1900
          |||||||
AL137471  198 TGATCTTGGAGAAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTFA 247

T416      1901 TTCTAGGAAGTTCCATAACTACATAATGTAACCATTGACCCATCTAATGGA 1950
          |||||||
AL137471  248 TTCTAGGAAGTTCCATAACTACATAATGTAACCATTGACCCATCTAATGGA 297

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FIG. 4A

FIG. 4B

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T416      2251 GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATAACCAACGT 2300
          |||||
AL137471  598 GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATAACCAACGT 647

T416      2301 TAGCATGGATTCTGTTCCTTACACAGAATGGGAGCTGTCTCAGTTATCATTC 2350
          |||||
AL137471  648 TAGCATGGATTCTGTTCCTTACACAGAATGGGAGCTGTCTCAGTTATCATTC 697

T416      2351 AGGACAAAAGGCAATCCTCAGCTACATACCAAAGTCCTTCTGAAGTGCAATG 2400
          |||||
AL137471  698 AGGACAAAAGGCAATCCTCAGCTACATACCAAAGTCCTTCTGAAGTGCAATG 747

T416      2401 ATCTTTGAATATGCAGAGTCGGTGACAAGTACAGCAATGACTTCAGTAAG 2450
          |||||
AL137471  748 ATCTTTGAATATGCAGAGTCGGTGACAAGTACAGCAATGACTTCAGTAAG 797

T416      2451 CCAGGCATCCTTGGATGCTCTCCATGATAATAATATTTCTTAGGAGCAA 2500
          |||||
AL137471  798 CCAGGCATCCTTGGATGCTCTCCATGATAATAATATTTCTTAGGAGCAA 847

T416      2501 TTTGTGCAGTGTGCTGGTTATTATGGTGCTATTTCGCAACTAGGTGTAAC 2550
          |||||
AL137471  848 TTTGTGCAGTGTGCTGGTTATTATGGTGCTATTTCGCAACTAGGTGTAAC 897

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FIG. 4C

T416	2551	CGCGAGAAAGACACTAGATCCTATAACTGCAGGGTGGCCGAATCAAC	2600
AL137471	898	CGCGAGAAAGACACTAGATCCTATAACTGCAGGGTGGCCGAATCAAC	947
T416	2601	TTACCAGCACCCCAAAGGCCATCCCGGCAGATTCACAAAGGGGACA	2650
AL137471	948	TTACCAGCACCCCAAAGGCCATCCCGGCAGATTCACAAAGGGGACA	997
T416	2651	TCACATTGGTGCTTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	2700
AL137471	998	TCACATTGGTGCTTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	1047
T416	2701	AGATCGTCTCCATCTTCATCTCCTACCTTAGAAAGAGGCAGATGGGCAG	2750
AL137471	1048	AGATCGTCTCCATCTTCATCTCCTACCTTAGAAAGAGGCAGATGGGCAG	1097
T416	2751	CCGGCAGAGTCACAACAGTCACCAGTCACCTCAACAGTTTGGTGACAATCT	2800
AL137471	1098	CCGGCAGAGTCACAACAGTCACCAGTCACCTCAACAGTTTGGTGACAATCT	1147
T416	2801	CATCAAACACGTGCCAGAGAAATTCTCATTAGAACTCACCCACGCCACT	2850
AL137471	1148	CATCAAACACGTGCCAGAGAAATTCTCATTAGAACTCACCCACGCCACT	1197

FIG. 4D

T416	2851	CCTGCTGTTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGGCA	2900
AL137471	1198	CCTGCTGTTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGGCA	1247
T416	2901	ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCAGGAGCTACA	2950
AL137471	1248	ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCAGGAGCTACA	1297
T416	2951	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCGT	3000
AL137471	1298	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCGT	1347
T416	3001	GGTGACAGTGAGGCAGGAGACAGTGATATGATTTGGGGCGAGATTCTCC	3050
AL137471	1348	GGTGACAGTGAGGCAGGAGACAGTGATATGATTTGGGGCGAGATTCTCC	1397
T416	3051	AATAGATAGGCTGCTGGGTGAAGGATTCAGCGACCTGTTTCTCACAGATG	3100
AL137471	1398	AATAGATAGGCTGTTGGGTGAAGGATTCAGCGACCTGTTTCTCACAGATG	1447
T416	3101	GAAGAAATTCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCTG	3150
AL137471	1448	GAAGAAATTCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCTG	1497

FIG. 4E

T416	3151	GGACACTCTGACCACTGCTGGATGCCACCACTGCCCTCACCGTCTTCTGA	3200
AL137471	1498	GGACACTCTGACCACTGCTGGATGCCACCACTGCCCTCACCGTCTTCTGA	1547
T416	3201	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAATTCCCAACGCAACCCC	3250
AL137471	1548	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAATTCCCAACGCAACCCC	1597
T416	3251	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	3300
AL137471	1598	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	1647
T416	3301	TCCGGTGAAAAGAAAGAGTTTTTCCACCTTTGGAAAGGACTCCCCAAA	3350
AL137471	1648	TCCGGTGAAAAGAAAGAGTTTTTCCACCTTTGGAAAGGACTCCCCAAA	1697
T416	3351	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	3400
AL137471	1698	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	1747
T416	3401	GCAGTGTGTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA	3450
AL137471	1748	GCAGTGTGTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA	1797

FIG. 4F

T416	3451	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCCTT	3500
AL137471	1798	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCCTT	1847
T416	3501	GCCAGCCAAAACCTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCA	3550
AL137471	1848	GCCAGCCAAAACCTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCA	1897
T416	3551	GTACGCATTTTCAAAATCCACCAACCACTGTGGGCCGCCACTTTGGAAC	3600
AL137471	1898	GTACGCATTTTCAAAATCCACCAACCACTGTGGGCCGCCACTTTGGAAC	1947
T416	3601	CACTCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	3650
AL137471	1948	CACTCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	1997
T416	3651	CCCTGAAAAATTATGAGGAAGATGATTTTGACAATGTGCTCAACCACCTCA	3700
AL137471	1998	CCCTGAAAAATTATGAGGAAGATGATTTTGACAATGTGCTCAACCACCTCA	2047
T416	3701	ATGATGGGAAACACGAACTCATGGATGCCAGTGAACCTGGTGGCAGAGATT	3750
AL137471	2048	ATGATGGGAAACACGAACTCATGGATGCCAGTGAACCTGGTGGCAGAGATT	2097

FIG. 4G

T416	3751	AACTGCTTCAAGATGTCCTCCGAGCTAGGAGATTTTAGCGAAGCA	3800
AL137471	2098	AACTGCTTCAAGATGTCCTCCGAGCTAGGAGATTTTAGCGAAGCA	2147
T416	3801	TTTTTGTTCATGTATATGGAATAGGAAACAACAACAACAAAAA	3850
AL137471	2148	TTTTTGTTCATGTATATGGAATAGGAAACAACAACAACAAAAA	2197
T416	3851	CCCTGAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC	3900
AL137471	2198	CCCTGAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC	2247
T416	3901	TGTGTATATTGAATATTAAATACTGTATTTTCGTATGTACACAAATGCAAG	3950
AL137471	2248	TGTGTATATTGAATATTAAATACTGTATTTTCGTATGTACACACAAAAA	2297
T416	3951	TGTGATTATTTTAATCTGTATTTTAAAAATACATTTGTACCTTATATTA	4000
AL137471	2298	AAAG.....	2338

FIG. 4H

T416	1	..ATGCACCAAAATG..AATGCTAAAAATGCACCTTTAGGTTTGTGTTTGGCA	45
m-PC	1	ATGATGCTACTTCTGCCATTCCCTGCTAGGGCTCTTAGGGCCAGGAAGCTA	50
T416	46	CTTCTGATAGTATCTTTCAACCAACGATGTACTGGGCA...AGAAATTTGAA	92
m-PC	51	CT..TGTTCAATTCAGGGGATTGTCAGGAGGTGGCCACTGTCATGGTGAA	98
T416	93	ATACAGGATTTATGAGGAAACAGAGGGTTGGATCAGTAATTGCAAGACTAT	142
m-PC	99	ATTCCAAGTGACAGAGGAAGTGCCGTCTGGCACGGTGATAGGGAAACTGT	148
T416	143	CAGAGGATGTGGCTGATGTTTATTGAAGCTTCCCTAATCCTTCTACTGTT	192
m-PC	149	CCCAAGAACT..AAGA.GTGGAGGAGAGGCGTGGGAAGGCAGGAGATG..	193
T416	193	CGATTTTCGAGCCATGCAGAGGGGAAATTCTCCTCTACTTGTAGTAAACGA	242
m-PC	194	CCTTCCAGATTCTGCAGCTGCCTCAGGCACCTGCCGGTTCAGATGAACCTC	242

FIG. 5A

T416	243	GGATAATGGGAAATCAGCATAGGGCTACAAATTGACCGTGAACAACTGT	292
m-PC	243	TGAGACGGCCTGCTCAGCACTTCCAGCCGGCTGGATCGGAGAAGCTAT	292
T416	293	GCCAGAAAAAAGTGAAGTGTTCATAGAGTTTGATGTGATCACTCTACCC	342
m-PC	293	GTCGGCAGGAAGATCCCTGTCTGGTGTCAATTGACGTG.....CTTGCC	336
T416	343	ACA.GAGCATCTGCAGCTTTTCCATATTTGAAGTTGAAGTGCTGGATATTA	391
m-PC	337	ACAGGGCGTCTGC.TCTAATTCAATGTGGAGATTCAGGTGCTAGACATCA	385
T416	392	ATGACAAATCTCCCCAGTTTTCAGATCTCTCATACCTATTGAGATATCT	441
m-PC	386	ATGACCACCAAGCCACAGTTTCCCAAGACGAGCAGGAAGTGGAAATCTCA	435
T416	442	GAGAGTGCAGCAGTTGGGACTCGCATTCCTCCCTGGACAGTGCAATTTGATCC	491
m-PC	436	GAGAGTGCCCTCTCTGCACACACAGAAATCCCTTTGGACAGAGCTCTTGACCA	485

FIG. 5B

T416	492	AGATGTTGGGGAATAATCCCTCCACACATACTCGCTCTCTGCCAATGATT	541
m-PC	486	AGACACGGGTCCTAACAGCTTATATTCTACTCCCTGTCTCCCAAGTGAAC	535
T416	542	TTTTTAATATCGAGGTTTCGACACAGGACTGATGGAGCCCAAGTATGCAGAA	591
m-PC	536	ACTTTGCCCTGGATGTTATTGTGGGCCCTGATGAGACCAAAACATGCAGAG	585
T416	592	CTCATAGTGGTCAGAGAGTTAGATCGGGAGCTGAAGTCAAGCTACGAGCT	641
m-PC	586	CTTGTGGTGGTGAAGGAGTTGGACAGGGAACCTCCACTCATATTTTGATCT	635
T416	642	TCAGCTCACTGCCCTCAGAC.ATGGGAGTACCTCAGAGGTCTGGCTCATCC	690
m-PC	636	GGTGTGACCGCCTATGACAAATGGGAAT.CCCCCTAAGTCAGGAATCAGC	684
T416	691	ATACTAAAAATAAGCATTTTCAGACTCCAATGACAAACAGCCCTGCTTTTGA	740
m-PC	685	GTGGTCAAGGTCAATGTCTCTGGACTCCAATGACAAATAGTCCAGTGTTC	734

FIG. 5C

T416	741	GCAGCAATCTTATATAAATACTCTTAGAAAACTCCCGGTTGGCACTT	790
m-PC	735	TGAGAGTTCACTAGCACTAGAAATCCAGAAAGACACTGTTCTCTGGTACTC	784
T416	791	TGCTCTTAGATCTGAATGCCACGGATCCAGATGAGGGCGCTAATGGAAA	840
m-PC	785	TTCTCATAAACCTGACTGCTACAGATCCCGACCAAGGACCCAAATGGGGAG	834
T416	841	ATTGTATATTCCTTCAGCAGTCA TG TGTCTCCCAAAATATGGAGACTTT	890
m-PC	835	GTAGAGTTCTTCTTTGGCAAGCATG TGTCCCCAGAGGTGATGAACACCTT	884
T416	891	TAAAAATTGATTCTGAAGAGGACATTTGACTCTTTTCAAGCAAGTGGATT	940
m-PC	885	TGGCATAGATGCCAAGACAGGCCAGATCATTTCTGCGCCAAGCCCTAGATT	934
T416	941	ATGAAATCACCAAATCCTATGAGATTGATGTTTCAGGCTCAAGATTTGGGT	990
m-PC	935	ACGAGAAGAACCCTGCCTATGAGGTGGATGTCCAGGCAAGGATTTGGGT	984

FIG. 5D

T416	991	CCAAATTCAATCCAGCCCATTTGCAAAATTATAATTAAAGTTGTGGATGT	1040
m-PC	985	CCCAATTCCATCCAGGCCATTGCAAAAGTTCTTATCAAAAGTTCTGGATGT	1034
T416	1041	TAATGACAATAAACCTGAAATTAAACATCAACCTCATGTCCCCTGGAAAAG	1090
m-PC	1035	CAATGACAATGCCCC.....AAGCATCCTCATCACGT....GGCCCTCC	1074
T416	1091	AAGAAATATCTTATATTTTGAAGGGGATCCTATTGATACATTTGTTGCT	1140
m-PC	1075	CAGACGTCGCT..GGTGTCAAGAAGATCTTCCAGGGATAGCTTCATTGCC	1122
T416	1141	TTGGTCAGAGTTCAGGACAAGGATTCTGGGCTGAATGGAGAAATAGTTTG	1190
m-PC	1123	CTTGTCAAGTGCGAATGACTTGGACTCAGGAACAACGGTCTCGTCCACTG	1172
T416	1191	TAAGCT...TCATGGACATGGTCACCTTAAACTTCAGAAAGACATATGAAA	1237
m-PC	1173	TTGGCTGAATCAAGAGCTGGGCCACTTCAGACTGAAAAGGACTAACGGCA	1222

FIG. 5E

T416 1238 ACAATTATTAACTTAACTAAATGCCACACTGGATAGAGAAAAGAGATCT 1287
 ||| || | | | | | | | | | | | | | | | |
 m-PC 1223 ACACGTACATGCTGCTCACCAATGCCACACTGGACAGAGAGCAGTGGCCC 1272

 T416 1288 GAGTATAGTTTGACTGTAATCGCTGAGGACAGGGGACACCCAGTC..TC 1335
 ||| | | | | | | | | | | | | | | | | |
 m-PC 1273 ATATATACTCTCACTGTGTGTTTGCCCAAGAC.CAAGGAC.CCCAGCCCTTA 1320

 T416 1336 TCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCAATGACAATCC 1385
 || | | | | | | | | | | | | | | | | | |
 m-PC 1321 TCAGCTGAGAAGGAGCTCCAAATTCAGGTTAGTGATGTCAATGACAATGC 1370

 T416 1386 ACCCCACTTCCAGAGAAGCCGATATGAATTTGTAATTTCAGAAAATAACT 1435
 || || | | | | | | | | | | | | | | | | |
 m-PC 1371 CCTGTGTTTGAGAAGAGCCGGTACGAGGTCTCCACTTGGGAAAATAACC 1420

 T416 1436 CACCAGGGGCATATATCACCACCTGTACAGCCACAGATCCTTGATCTTGGA 1485
 ||| | | | | | | | | | | | | | | | | |
 m-PC 1421 CACCCTCTCTTCAACCTCATCAGCTCAAAGCGCATGATGCTGACTTGCGC 1470

FIG. 5F

T416	1486	GAAAATGGGCAAGTGACATACACCATCTTGGA.GAGTTTATTCT.AGGA	1533
m-PC	1471	AGTAATGGAAAAGTGTATACCGTATCAAGGACTCCCCCGTTTCTCACTT	1520
T416	1534	AGTTCCTAACTACATATGTAACCATTTGA...CCCATCTAATGGAGCCAT	1580
m-PC	1521	AGT..CATTATTGACTTTGAAACAGGAGAAGTCACTGCTCAGAGGTCACT	1568
T416	1581	...CTATGCC...TCAGAAATCTTTGA..TC...ATGA.AGAAGTGAGTC	1618
m-PC	1569	GGACTATGAACAGATGGCAGGCTTTGAGTTCAGGTGATAGCAGAG.GAC	1617
T416	1619	AGATCAC.TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCGAAGCAACT	1667
m-PC	1618	AGAGGGCAACCCAGCTCGCATCCAG.CATCTCGGTGTGGTTAGCCCTCT	1666
T416	1668	GGTAAGC.....AATACCACAGTTGTG.CTCACC.....ATCATTTGAC	1704
m-PC	1667	TGGATGCCCAATGATAATGCCCCCAGAAGTGATTACGCCCTGTGCTCAGTGAA	1716

FIG. 5G

T416	1705	GAAAATGACAACGTTCTGTGGTTATA.....GGGCC.....	1736
m-PC	1717	GGCAAAGCCACCCCTTTCGGTGTCTGTAAATGCCCTCCACGGGCCACCTTCT	1766
T416	1737	..TG..CATTCGGTA.....AT.AATACGGCAGAAATCACCATTC	1771
m-PC	1767	GTGCCCCATTGAGAAATCCCAGTGGCATGGATCCAGCAGGTACTGGTATAC	1816
T416	1772	..CCAAAGG.GGCTGAAAG....TGG.CTTT.CATGTCACAAGAATAAGG	1812
m-PC	1817	CACCAAAGGCTACCCACAGCCCCCTGGTCTTTCCTTTTGTAAACAATCGTG	1866
T416	1813	GCAATTGACAGAGACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCATAGT	1862
m-PC	1867	GCTAGGGATGCAGACTCGGGGCCAATGGGGAACCTTCTACAGCATTCA	1916
T416	1863	AGCAGGTAATGAGGAGAAATATCTTCATAATTGATCCACGATCATGTGACA	1912
m-PC	1917	AAGTGGGAATGATGCTCATCTCTT.TTTCCTCAGCC.CTTCCCTTGGGGCA	1964

FIG. 5H

T416	1913	TCCAT..ACCAACGTTAGC.ATGGATTCTGTCCCTACACAG..AATGGG	1957
m-PC	1965	GCTATTCAATTAAATGTCACCAATGCCAGCAGCCTCATCGGAGTCAGTGGG	2014
T416	1958	AGCTGTCAGTTATCATTCAGGACAAAGGCAATCCTCAGCTACATACCAA	2007
m-PC	2015	ACCTGGGATAGTGGTAGAGGACCAGGGCAGCCCTCCTTGCAGACCCAA	2064
T416	2008	GTCCTTCTGAAGTGCATGATCTTTGAAATATGCAGAGTCGGTGACAAGTAC	2057
m-PC	2065	GTTTCATTGAAGGTCGTG...TTTG..TCACCAGTGT..GGACCACCTAA	2107
T416	2058	AGCAATGACTTCAGTAAGCCAGGCATCCTTGGATGTCCTCCATGA.TAATA	2106
m-PC	2108	GGGATTCTGCTCA.TGAGCCCGGAGTTCT..GAGCACACCAGCAGCCTGGCT	2154
T416	2107	ATTATTTCCTTAGGAGCAATTGTGCAGTGTGCTGGTTATTATGGTGCT	2156
m-PC	2155	TTGATCTGCCCTGGCTGTACTGCTGGCCATCTTTGGATTGCTCTTAGCCCT	2204

FIG. 5I

T416	2157	ATTGCAACTAGGTGTAACCGCGAGAGAAAGACACTAGATCCTATAACT	2206
m-PC	2205	GTTCGTGTCCATCTGCAGGACAGAGAGAAAGGATAATAGGGCCTACAAC	2254
T416	2207	GCAGGGTGGCCGAATCAACTTACCAGCACCCCAAAAAGGCCATCCCGG	2256
m-PC	2255	GTCGAGAAAGCTGAGTCGTGTCATACCGCCACAGCCCAAGAGGCCCCAGAAA	2304
T416	2257	CAGATTCACAAAGGGGACATCACATTGGTGCCCTACCATAAATGGCACTCT	2306
m-PC	2305	CACATTCAGAAGGCAGATATCCACCTGGTGCCCTGTGCT.TAGGGCCCCAC.	2352
T416	2307	GCCCATCAGATCTCATCA...CAGATCGTCTC.CATCTTCATCTCCTA..	2350
m-PC	2353	GAGAAATGAGA.CTGATGAAGTCAGGCCCATCTCACAAGGATACCAGCAAG	2401
T416	2351	..CCTTAGAAAGAGGGCAGATGGG.....CAGCCGGCAGAGTCACAA	2390
m-PC	2402	AGACACTGATGGAGGCAGGCTGGGACTCTTGCCCTGGAGGCCCCCTTCCAC	2451

FIG. 5J

T416	2391	CAGTCACCAGTCACTCAACAGTTTGGTGACAATCTCATCAAACCACG...	2437
m-PC	2452	CTCACACCA.ACCCTATACAGGACCCCTGCGTAACCAAGGCAACCAGGGAG	2500
T416	2438	...TGCCAGA.....GAATTCTTCT.CATTAGAAC.TCACC...CACGCC	2472
m-PC	2501	AACTGGCAGAGAGCCAGGAGGTACTGCAGGACACCTTCAACTTCTCTTT	2550
T416	2473	ACTCCTGC..TGTTGA.GCAGGTCTCTC...AGCTTCT...TTCAATGC	2512
m-PC	2551	AACCATCCAGGCAGAGGAATGCCTCCCGGAGAACCTAAACCTTCCTGA	2600
T416	2513	TTCAACCAGGGCAATA..TCAGCCAAGACCAAG..TTTTCGAGGAAACAA	2558
m-PC	2601	GTCCCCACCTGCTGTACGCCAACCACTCTTAAGGCCCTCTGAAGGTGCCCTG	2650
T416	2559	ATATTCCAGGAGCTACAGATA.TGCCCTTCAAGACATGGACAAATTTAGC	2607
m-PC	2651	GTAGCCCCATAGCGAGGGCGACTGGAGACCAAGACAAAGGAGGA....GGC	2696

FIG. 5K

T416	2608	TTGAAAGACAGTGGCCGTGGTGACAGTGAGGC..AGGAGACAG.TGATTA	2654
m-PC	2697	CCCACAGAGCCCAACAGCGTCCCTCTGCAACCCCTAAGACGACAGCGGAATT	2746
T416	2655	TGATTTGGGGCGAGATTCTCCAATA.GATAGGCTGCTGGGTGAAGGATTC	2703
m-PC	2747	TCAAT..GGCAAAGTGTCTCCTAGAGGAGAGTCCGGTCCCTCATCAGATTC	2794
T416	2704	..AGCGACCTGTTT...CTCACAGATGGAAGAAATTCAGCAGCTATGAGA	2748
m-PC	2795	TGAGGAGCCTGGTTAGGCTCTCTG.TGGCTGCTTTTGCGGA...ACGGAA	2840
T416	2749	CTCTGCACGGAGGAG..TGCAGGGTCCTGGGACACTCTGACCAGTGCTGG	2796
m-PC	2841	CCCGG..TGGAGGAGCCTGCTGGGACT..CTCCTCCTGTCCAGCAAATC	2886
T416	2797	ATGCCACCACTGCCCTCAC....CGTCTTCTGATTATAGGAGTAACATGT	2842
m-PC	2887	TCCCAGCTGCTGTCTTGTCTGCACACGAGGCCAATTCACAGCCCAACCAAA	2936

FIG. 5L

T416	3083	AGGTGGATCG.GTCCAACTCCCTGGAGCGCAGGAAGGACCCCTTGCCAGC	3131
m-PC	3172	GCCTGGATGGCGAGATTGTCAATTGCCCCCTCA.....CCACCAATTATCGA	3216
T416	3132	CAAAACTGTGGGTTACCCACAGGGGTAGCGGCATGGGCAGCCAGTACGC	3181
m-PC	3217	GACAACT.TGTCTTCCCCCGATGCTACAACATCAGAGGAACCGAGAAC..	3263
T416	3182	ATTTTCAAAATCCCAACCACTGTGGCCGCCACTTGGAACCTCACTCC	3231
m-PC	3264	.CTTCCAGACATTTCGGCAAGACAGTTGGACCGGGAC.CCGAGCTGAGCCC	3311
T416	3232	AGTGTGCAGCCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGATCCCT..	3279
m-PC	3312	AACAGGCACGGCCTGGCCAGCACTTTCGTCTCGGAGATGAGCTCTCTGC	3361
T416	3280	..GAAA..ATTATGAGGAAGATGATTTTGACAAATG..TGCT.CAACCACC	3322
m-PC	3362	TGGAATGTTGTTGGGGCAGCACACGGTACCAGTGGAGCTGCGTCCGCG	3411

FIG. 5N

T416	3323	TCAATGATGGGAAACACGAACTCATGGATG....CCAGT...GA.....	3359
m-PC	3412	GCTTTGCGGAGGCTCTCGGTGTGCGGAGGACCCCTCAGTCTAGACCTAGC	3461
T416	3360ACTGGTGGCAGAGATTAACAA..ACTGCTT..CAAGATGTCCGC.C	3400
m-PC	3462	CACCAAGTGGGGCTTCAGCTTCAGAAAGCACAGGTTAGAAAGGAGGAGCTG	3511
T416	3401	AGAGC.....	3405
m-PC	3512	AGAGCAGACTTGGCTGTGGCAGGAATCTA	3540

FIG. 50

m-PC	1	MMLLLPFLGLLGPGLSFLISGDCQEVATVMVKFQVTEEVPSGTVIGKLS	50
T416	1	.MHQMNAKMHFRFVFALLIVSFN.HDVLGKNLKYRIYEEQRVGSVIARLS	48
m-PC	51	QELR..VEERRGKAGDAFQILQLPQALPVQMNSEDGLLSTSSRLDREKLC	98
T416	49	EDVADVLLKLPNPSTVFRAMQRGNSPLLNVNEDNGEISIGATIDREQLC	98
m-PC	99	RQEDPCLVSFDV..LATGASALIHVEIQVLDINDHQPPQFPKDEQELEISE	146
T416	99	QKNLNCSEFDVITLPTTEHLQLFHIEVEVLDINDNSPQFSRSLPIEISE	148
m-PC	147	SASLHTRIPLDRALDQDTGPNLSYSLSLSPSEHFALDVI VGPDETKHAEL	196
T416	149	SAAVGTRIPLDSAFDPDVGENSLHTYLSLSANDFFNIEVRTRTDGAKYAEL	198
m-PC	197	VVKELDRELHSYFDLVLTAYDNGNPPKSGISVVKVNVLDNSDNDNSPVFAE	246
T416	199	IVVRELDRELKSSYELQLTASDMGVQPQRSGSSILKISISDSNDNSPAFEQ	248

FIG. 6A

m-PC	247	SSLALEIPEDTVPGTLLINLTATDPDQGPNGEVEFFGKHVSPEVMNTFG	296
T416	249	QSYIIQLENSPVGTTLLDLNATDPDEGANGKIVYSFSSHVSPKIMETFK	298
m-PC	297	IDAKTGQIILRQALDYEKNPAYEVDVQARDLGPNSIPGHCKVLIKVLDVN	346
T416	299	IDSERGHLTLFKQVDYEITKSYEIDVQAQDLGPNSIPAHCKIILKVVDVN	348
m-PC	347	DNAPSILITWAS...QTSLVSEDLPRDSFIALVSANDLDSGNNGLVHCW	392
T416	349	DNKPEININLMSGKEEISYIFEGDPIDTFVALVRVQDKDSGLNGEIVCK	398
m-PC	393	LNQELGHFRLKRTNGNTYMLLTNATLDREQWPIYTTLTVFAQDQGPQLSA	442
T416	399	LHGH.GHFKLQKTYENNYLILTNAATLDREKRSEYSLTVAEDRGTPSLST	447
m-PC	443	EKELQIQVSDVNDNAPVFEKSRYEVSSTWENNPPSLHLITLKAHDADLGSN	492
T416	448	VKHFTVQINDINDNPPHFQRSRYEFVISENNSPGAYITTVTATDPDLGEN	497

FIG. 6B

m-PC	493	GKVSRIKD.....SPVSHLVIIDFETGEVTAQRSLDYEQMAGFEFQVIA	537
T416	498	GQVTYTILESFILGSSITTYVTIDPSNGAIYALRIFDHEEVSQITFVVEA	547
m-PC	538	EDRGQP.QLASSISVWVSLLDANDNAPEVIQPVLSE GKATLSVLVNASTG	586
T416	548	RDGSPKQLVSNNTTVVLTIIENDNVVVGIPALRNNTAEITIPKGAESG	597
m-PC	587	HLLLPINPSGMDPAGTGIPPKATHSPWSFLLTTIVARDADSGANGELFY	636
T416	598FHVTRIRAIDRDSGVNAELSC	618
m-PC	637	SIQSGNDAHLFFLSPSLGQLFINVTNASSLLIGSQWDLGIVVEDQGSPSLQ	686
T416	619	AIVAGNEENIFIIDPRSCDIHTNV.SMDSVPYTEWELSVIIQDKGNPQLH	667
m-PC	687	TQVSLKV...FVTSVDHLRDSAHEPGVLSTPALALICLAVLLAIFGLLL	733
T416	668	TKVLLKCMIFEYAESVTSTAMTSVSQASLDVSMIIISLGAICAVLLVIM	717

FIG. 6C

m-PC	734	ALFVSI	CRTERK	DNRAYN	CREAES	SYRHQP	KRPQKH	IQAD	IHLV	PVLR	A	783
T416	718	VLFAT	RNCN	REKKD	TRSYN	CRVAE	STYQH	HPKR	PSRQ	IHKG	DITL	767
m-PC	784	HENET	DEV	..PSH	KDTSK	ETLME	AGWD	SCLE	APFH	LTP	TL	831
T416	768	TLPIR	SHR	SSP	SSPT	L	ERGQ	MGSR	QSHN	SHQ	SLN	817
m-PC	832	QGE	LAES	QEV	LQD	T	FN	FLN	HPRQ	NA	REN	881
T416	818	SLE	LTHA	TPA	VEQ	V	SQ	LLS	MLH	QGYQ	P	867
m-PC	882	VPG	PIA	RAT	G	QD	K	E	E	A	P	931
T416	868	FS...	LKD	S	GRGD	SE	AGD	S	DYD	LGRD	S	913
m-PC	932	L	R	S	L	V	R	L	S	V	A	981
T416	914	A	M	R	L	C	T	E	E	C	R	963

FIG. 6D

m-PC	982	GNKYLAKPGSSRG	TIPDTEGLVGL.KPSGQAE	PDL	EEGPPSP	PEEDLSVK	1030	
T416	964	HQLEDDAQPADS	GEKKKSFSTFGK	DSPN	DEDTGDTST	SLLSEMSSVFQ	1013	
m-PC	1031	RLLEEL...	SSLLDPNTGLALDKL	SPDP	PAWMARLSL	PLTTNYRDN	LSS 1077	
T416	1014	RLPPSLD	TYSECSEVDR	NSLER	RKGPLPA	KTVGYPQGV	AAWAASTHFQ 1063	
m-PC	1078	PDATTSEEP	RTFQTFGKTV	CGPELSPTG	TRLLASTFV	SEMSSLLEML	LQG 1127	
T416	1064	NPTTCGP	PLGTHS...SVQP	SSKWLPA	MEIIPENY	EEDDDFN	VNLHND 1110	
m-PC	1128	HTVPVEA	ASAALRR	LSVCGRTL	SLDLATSG	ASAEAQGR	KKAESRLGCC	RNL 1180
T416	1111	GKHELM	DASELVAE	INKLLQD	VRQS.....			1135

FIG. 6E

GAAGTGGGAT	GTGCAAAAGC	GCCGGCTGGA	AATCCCGGCT	GTGTCTCCGT	CAACTCTTTA	60
CGCAACAGAG	GTCTCCCCCT	GCCCTTGGTT	TCTACCGGGC	CGCCTGCTCC	CACTCGGCGA	120
AAAAAATTAC	ACAACAGCAG	CCGCGGCG	ATG ACG	TGG AGG	GCT GCC	172
	Met Thr	Trp Arg	Ala Ala	Ala Ser		8
ACG TGC	GCG CTC	CTG ATT	CTG CTG	TGG GCG	CTG ACC	GAA GGT
Thr Cys	Ala Ala	Leu Leu	Ile Leu	Trp Ala	Leu Thr	Thr Glu Gly
						24
GAT CTG	AAA GTA	GAG ATG	GCA GGG	GGG ACT	CAG ATC	ACA CCC
Asp Leu	Lys Val	Glu Met	Met Ala	Gly Thr	Gln Ile	Thr Pro Leu
						40
AAT GAC	AAT GTC	ACC ATA	TTC TGC	AAT ATC	TTT TAT	TCC CAA
Asn Asp	Asn Val	Thr Ile	Phe Thr	Cys Asn	Ile Phe	Tyr Ser
						Gln Pro Leu
						56
AAC ATC	ACG TCT	ATG GGT	ATC ACC	TGG TTT	TGG AAG	AGT CTG
Asn Ile	Thr Ser	Met Gly	Ile Thr	Trp Phe	Trp Lys	Ser Leu
						Thr Phe
						72
GAC AAA	GAA GTC	AAA GTC	TTT GAA	TTT TTT	GGA GAT	CAC CAA
Asp Lys	Glu Glu	Val Lys	Val Phe	Phe Phe	Gly Asp	His Gln
						Glu Ala
						88
TTC CGA	CCT GGA	GCC ATT	GTG TCT	CCA TGG	AGG CTG	AAG AGT
Phe Arg	Pro Pro	Gly Ala	Ile Val	Ser Pro	Trp Arg	Leu Lys
						Ser Gly Asp
						104
GCC TCA	CTG CGG	CTG CCT	GGA ATC	CAG CTG	GAG GAA	GCA GGA
Ala Ser	Leu Arg	Leu Pro	Gly Ile	Gln Leu	Glu Glu	Ala Gly
						Glu Tyr
						120

Fig. 7A

CGA	TGT	GAG	GTG	GTG	GTC	ACC	CCT	CTG	AAG	GCA	CAG	GGA	ACA	GTC	CAG	556
Arg	Cys	Glu	Val	Val	Val	Thr	Pro	Leu	Lys	Ala	Gln	Gly	Thr	Val	Gln	136
CTT	GAA	GTT	GTG	GCT	TCC	CCA	GCC	AGC	AGA	TTG	TTG	CTG	GAT	CAA	GTG	604
Leu	Glu	Val	Val	Ala	Ser	Pro	Ala	Ser	Arg	Leu	Leu	Leu	Asp	Gln	Val	152
GGC	ATG	AAA	GAG	AAT	GAA	GAC	AAA	TAT	ATG	TGT	GAG	TCA	AGT	GGG	TTC	652
Gly	Met	Lys	Glu	Asn	Glu	Asp	Lys	Tyr	Met	Cys	Glu	Ser	Ser	Gly	Phe	168
TAC	CCA	GAG	GCT	ATT	AAT	ATA	ACA	TGG	GAG	AAG	CAG	ACC	CAG	AAG	TTT	700
Tyr	Pro	Glu	Ala	Ile	Asn	Ile	Thr	Trp	Glu	Lys	Gln	Thr	Gln	Lys	Phe	184
CCC	CAT	CCC	ATA	GAG	ATT	TCT	GAG	GAT	GTC	ATC	ACT	GGT	CCC	ACC	ATC	748
Pro	His	Pro	Ile	Glu	Ile	Ser	Glu	Asp	Val	Ile	Thr	Gly	Pro	Thr	Ile	200
AAG	AAT	ATG	GAT	GGC	ACA	TTT	AAT	GTC	ACT	AGC	TGC	TTG	AAG	CTG	AAC	796
Lys	Asn	Met	Asp	Gly	Thr	Phe	Asn	Val	Thr	Ser	Cys	Leu	Lys	Leu	Asn	216
TCC	TCT	CAG	GAA	GAC	CCT	GGG	ACT	GTC	TAC	CAG	TGT	GTG	GTA	CGG	CAT	844
Ser	Ser	Gln	Glu	Asp	Pro	Gly	Thr	Val	Tyr	Gln	Cys	Val	Val	Arg	His	232
GCG	TCC	TTG	CAT	ACC	CCC	TTG	AGG	AGC	AAC	TTT	ACC	CTG	ACT	GCT	GCT	892
Ala	Ser	Leu	His	Thr	Pro	Leu	Arg	Ser	Asn	Phe	Thr	Leu	Thr	Ala	Ala	248
CGG	CAC	AGT	CTT	TCT	GAA	ACT	GAG	AAG	ACA	GAT	AAT	TTT	TCC	ATT	CAT	940
Arg	His	Ser	Leu	Ser	Glu	Thr	Glu	Lys	Thr	Asp	Asn	Phe	Ser	Ile	His	264

Fig. 7B

TGG TGG CCT ATT TCA TTC ATT GGT GTT GGA CTG GTT TTA TTA ATT GTT	988
Trp Trp Pro Ile Ser Phe Ile Gly Val Gly Leu Val Leu Leu Ile Val	280
TTG ATT CCT TGG AAA AAG GTA AGG GGC TCC AAA GCA AAG TTC AGC CCT	1036
Leu Ile Pro Trp Lys Lys Val Arg Gly Ser Lys Ala Lys Phe Ser Pro	296
GTG TCT TGG GCT AGT AAA AAG CTT TTA GAG CAG CTG CTG CCA ACC TTA	1084
Val Ser Trp Ala Ser Lys Lys Leu Leu Glu Gln Leu Leu Pro Thr Leu	312
CAA GCC TCA AGG GAC AGG CCT GCT GGA AAG GAC TTT GTC AGT CCC TCT	1132
Gln Ala Ser Arg Asp Arg Pro Ala Gly Lys Asp Phe Val Ser Pro Ser	328
TCA CCA TCA GGT GTT GGG AAT GTT GGC TGT GTT CCA ATC CAG TTT CCT	1180
Ser Pro Ser Gly Val Gly Asn Val Gly Cys Val Pro Ile Gln Phe Pro	344
ATC ACA GAG GAC CTA GCT GTC ACA TAC CAT CTG ACC TCT GTA TGG TGG	1228
Ile Thr Glu Asp Leu Ala Val Thr Tyr His Leu Thr Ser Val Trp Trp	360
TTT GTG ACT CTG GGG TGATGTGTTG TAAAGCCTCC CTCTCTTTCT CCATACTAAA	1283
Phe Val Thr Leu Gly	365
CAAGTATTAT ATCTCTGTGA ATGAACCAGA CTTTAGTGTT CAGACCAGGC CCTGAACCTAT	1343
GTGTGGACTG CTTGTTTTTC TCACACATTT AGAAACTATG GCTTAGAGAG GGAATTCCT	1403
CATATTTTAT CTGATCAATA ACTGACCACC AGATCTCACT AGTTTGACTA AGAATTTCTA	1463
ACCCTCACTA GGTATTCTA AACTAAAACA TGTTTCTAAA CATTTTATC CCTGACTATG	1523

Fig. 7C

GCCCAAATAG	TAAATAAAC	AGCTCAAGCT	TTAGAGGCCC	AAGAGACCTA	TGTAATGTG	1583
TTGGTTAAAA	TAGTTT TAGA	TAATAAAAGG	GCCCTCAATT	ATTTATGGGC	CTGTCAAGGC	1643
AAAATCTGCA	CAACAGCCAG	TACATCTCAT	TATAAATAAT	TTAGGAGAAG	TGGAATAATC	1703
AGTCAATTA	GAAAAATGGC	CCTTTATCTA	AAGTTGGCCA	TTTAGATTCA	CGGACTTAT	1763
TCCTGTTGGA	TCTAGGCCAT	GAGAAAAC TG	GATAAAAAGT	GGTTTTCAAA	TGTTTCTTGT	1823
GGTATTTGTG	ACTGTTGTCA	TATTTCTTGC	CTTCTCTCTGG	TTCTGATATT	CAGGTGCTAT	1883
TGAGAGAGGA	GGAAGGAAGA	AACTAGTCAG	GCAGGCAGTT	AGGGTGGGCC	CTCAGTCAAA	1943
TTCCCTTCAA	CAAAAGAAC	GCCTGAAAAA	TCAAAC TGCA	GATAAGGGAA	CTTGTAACAGG	2003
GGGGCTTGCC	TAAACATGC	CCACAGCCAC	ATACATTAAA	ACAAGGCTAC	ACAGGAGACT	2063
TGCCTAGACA	TGCTCACAAT	AGAAAATTCC	ATCCCCTGAC	ACATGCACAG	TAAGGGGAAC	2123
AAAGCCACAT	GGAGTAACTC	AAGCTAAGGG	CTTGCA TGCA	CACTACGAGG	ATGGGTGGA	2183
GCTACCAGAA	ATGTGTGCCT	TATGCCTTTG	TATTCAGCTG	TGAAAATGGCA	ACCCCTCTTTT	2243
GGGCCCCCTC	TCTGCAGTGG	AGTGCTTTCT	TCTTTTGCTT	ATTAAACTTT	CACTTCAACT	2303
TCAAAAAAAA	AAAAAAA	AAAAAAA				2330

Fig. 7D

GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	2246
GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	121136
CAAAAAGAGG	GTTGCCATTT	CACAGCTGAA	TACAAAGGCA	TAAAGGCACAC	ATTTCTGGTA	2186
CAAAAAGAGG	GTTGCCATTT	CACAGCTGAA	TACAAAGGCA	TAAAGGCACAC	ATTTCTGGTA	121196
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	2126
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	121256
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCCTAGG	2066
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCCTAGG	121316
CAAGTCTCCT	GTGTAGCCTT	GTTTAAATGT	ATGTGGCTGT	GGGCATGTTT	TAGGCAAGCC	2006
CAAGTCTCCT	GTGTAGCCTT	GTTTAAATGT	ATGTGGCTGT	GGGCATGTTT	TAGGCAAGCC	121376
CCCCGTGACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	1946
CCCCGTGACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	121436

Fig. 9A

AATTGACTG	AGGGCCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCTT	CCTCCTCTCT	1886
AATTGACTG	AGGGCCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCTT	CCTCCTCTCT	121496
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGGCAAGAAA	TATGACAACA	GTCACAAAATA	1826
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGGCAAGAAA	TATGACAACA	GTCACAAAATA	121556
CCACAAGAAA	CATTTGAAAA	CCACTTTTTA	TCCAGTTTTT	TCCATGGCCTA	GATCCAACAG	1766
CCACAAGAAA	CATTTGAAAA	CCACTTTTTA	TCCAGTTTTT	TCCATGGCCTA	GATCCAACAG	121616
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	1706
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	121676
CTGATTATTC	CACCTCTCCT	AAATTATTTA	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	1646
CTGATTATTC	CACCTCTCCT	AAATTATTTA	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	121736
TTGCCCTTGAC	AGGCCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	1586
TTGCCCTTGAC	AGGCCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	121796

Fig. 9B

AACACATT	TA	CTGTTT	TATT	TACTATT	TGG	1526
AACACATT	TA	CTGTTT	TATT	TACTATT	TGG	121856
GCCATAGT	CA	CTGTTT	TAG	CCTAGT	GAGG	1466
GCCATAGT	CA	CTGTTT	TAG	CCTAGT	GAGG	121916
GTTAGAAA	TT	CTGTTT	GATC	AGATAAA	ATA	1406
GTTAGAAA	TT	CTGTTT	GATC	AGATAAA	ATA	121976
TGAGGAAT	TC	CTAAAT	GTGT	GAGAAAA	ACAGTCC	1346
TGAGGAAT	TC	CTAAAT	GTGT	GAGAAAA	ACAGTCC	122036
ACATAGTT	CA	AGTCTG	GTTC	ATTCAC	AGATATA	1286
ACATAGTT	CA	AGTCTG	GTTC	ATTCAC	AGATATA	122096
TGTTTAGT	AT	CACCC	CAGAG	TCACAA	ACCA	1226
TGTTTAGT	AT	CACCC	CAGAG	TCACAA	ACCA	122156

Fig. 9C

CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	1166
CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	122216
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCCAGC	1106
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCCAGC	122276
AGGCCTGTCC	CTTGAGGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	1046
AGGCCTGTCC	CTTGAGGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	122336
CCAAGACACA	GGGCTGAACT	TTGCTTTGGA	GCCCTTACC	TTTTTCCAAG	GAATCAAAAC	986
CCAAGACACA	GGGCTGAACT	TTGCTTTGGA	GCCCTTACC	TTTTTCCAAG	GAATCAAAAC	122396
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGGAAAAATT	926
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGGAAAAATT	122456
ATCTGTCTTC	TCAGTTTCAG	AA				904
ATCTGTCTTC	TCAGTTTCTG	CA				122478

Fig. 9D

GGCCCCGGCAGCTCGGGCTCGGGATCCGTCGAGGGGAGGCCGAGCTTGCCAAGCTGGCGCCAGCGGGGTC	M	V	2
		ATG	77
P G A R G G A L A R A A G R G L L A L			22
CCC GGC GCC CGC GGC GGC GCA CTG GCG GGT GCT GCC GGC GGC CTC CTG GCT TTG			137
L L A A V S A P L R L Q A E E L G D G C G			42
CTG CTC GCG GTC TCC GCC CCG CTC CCG CTG CAG GCG GAG GAG CTG GGT GAT GGC TGT GGA			197
H L V T Y Q D S G T M T S K N Y P G T Y			62
CAC CTA GTG ACT TAT CAG GAT AGT GGC ACA ATG ACA TCT AAG AAT TAT CCC GGC ACC TAC			257
P N H T V C E K T I T V P K G K R L I L			82
CCC AAT CAC ACT GTT TGC GAA AAG ACA ATT ACA GTA CCA AAG GGC AAA AGA CTG ATT CTG			317
R L G D L D I E S Q T C A S D Y L L F T			102
AGG TTG GGA GAT TTG GAT ATC GAA TCC CAG ACC TGT GCT TCT GAC TAT CTT CTC TTC ACC			377
S S S D Q Y G P Y C G S M T V P K E L L			122
AGC TCT TCA GAT CAA TAT GGT CCA TAC TGT GGA AGT ATG ACT GTT CCC AAA GAA CTC TTG			437
L N T S E V T V R F E S G S H I S G R G			142
TTG AAC ACA AGT GAA GTA ACC GTC CGC TTT GAG AGT GGA TCC CAC ATT TCT GGC CGG GGT			497

Fig. 10A

F L L T Y A S S D H P D L I T C L E R A 162
TTT TTG CTG ACC TAT GCG AGC AGC GAC CAT CCA GAT TTA ATA ACA TGT TTG GAA CGA GCT 557

S H Y L K T E Y S K F C P A G C R D V A 182
AGC CAT TAT TTG AAG ACA GAA TAC AGC AAA TTC TGC CCA GCT GGT TGT AGA GAC GTA GCA 617

G D I S G N M V D G Y R D T S L L C K A 202
GGA GAC ATT TCT GGG AAT ATG GTA GAT GGA TAT AGA GAT ACC TCT TTA TTG TGC AAA GCT 677

A I H A G I I A D E L G G Q I S V L Q R 222
GCC ATC CAT GCA GGA ATA ATT GCT GAT GAA CTA GGT GGC CAG ATC AGT AGT GTG CTT CAG CGC 737

K G I S R Y E G I L A N G V L S R D G S 242
AAA GGG ATC AGT CGA TAT GAA GGG ATT CTG GCC AAT GGT GTT CTT TCG AGG GAT GGT TCC 797

L S D K R F L F T S N G C S R S L S F E 262
CTG TCA GAC AAG CGA TTT CTG TTT ACC TCC AAT GGT TGC AGC AGA TCC TTG AGT TTT GAA 857

P D G Q I R A S S S W Q S V N E S G D Q 282
CCT GAC GGG CAA ATC AGA GCT TCT TCC TCA TGG CAG TCG GTC AAT GAG AGT GGA GAC CAA 917

V H W S P G Q A R L Q D Q G P S W A S G 302
GTT CAC TGG TCT CCT GGC CAA GCC CGA CTT CAG GAC CAA GGC CCA TCA TGG GCT TCG GGC 977

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Fig. 10B

Sequence

D S S N N H K P R E W L E I D L G E K K 322
 GAC AGT AGC AAC AAC CAC CAC AAA CCA CGA GAG TGG CTG GAG ATC GAT TTG GGG GAG AAA AAG 1037

 K I T G I R T T G S T Q S N F N F Y V K 342
 AAA ATA ACA GGA ATT AGG ACC ACA GGA TCT ACA CAG TCG AAC TTC AAC TTT TAT GTT AAG 1097

 S F V M N N F K N N S K W K T Y K G I V 362
 AGT TTT GTG ATG AAC TTC AAA AAC AAT AAT TCT AAG TGG AAG ACC TAT AAA GGA ATT GTG 1157

 N N E E K V F Q G N S N F R D P V Q N N 382
 AAT AAT GAA GAA AAG GTG TTT CAG GGT AAC TCT AAC TTT CGG GAC CCA GTG CAA AAC AAT 1217

 F I P P I V A R Y V R V V P Q T W H Q R 402
 TTC ATC CCT CCC ATC GTG GCC AGA TAT GTG CGG GTT GTC CCC CAG ACA TGG CAC CAG AGG 1277

 I A L K V E L I G C Q I T Q G N D S L V 422
 ATA GCC TTG AAG GTG GAG CTC ATT GGT TGC CAG ATT ACA CAA GGT AAT GAT TCA TTG GTG 1337

 W R K T S Q S T S V S T K K E D E T I T 442
 TGG CGC AAG ACA AGT CAA AGC ACC AGT GTT TCA ACT AAG AAA GAA GAT GAG ACA ATC ACA 1397

 R P I P S E E T S T G I N I T T V A I P 462
 AGG CCC ATC CCC TCG GAA GAA ACA TCC ACA GGA ATA AAC ATT ACA ACG GTG GCT ATT CCA 1457

Fig. 10C

L	V	L	L	L	V	V	L	V	F	A	G	M	G	I	F	A	A	F	R	K	482
TTG	GTG	CTC	CTT	GTT	GTC	CTG	CTG	GTG	TTT	GCT	GGA	ATG	GGG	ATC	TTT	GCA	GCC	TTT	AGA	AAG	1517
K	K	K	K	G	S	P	P	Y	G	S	A	E	A	Q	K	T	D	C	W	K	502
AAG	AAG	AAG	AAA	GGA	AGT	CCG	TAT	GGA	TCA	GCA	GAG	GCT	CAG	AAA	ACA	GAC	TGT	TGG	AAG	1577	
Q	I	K	Y	P	F	A	R	H	Q	S	A	E	F	T	I	S	Y	D	N	522	
CAG	ATT	AAA	TAT	CCC	TTT	GCC	AGA	CAT	CAG	TCA	GCT	GAG	TTT	ACC	ATC	AGC	TAT	GAT	AAT	1637	
E	K	E	M	T	Q	K	L	D	L	I	T	S	D	M	A	D	Y	Q	Q	542	
GAG	AAG	GAG	ATG	ACA	CAA	AAG	TTA	GAT	CTC	ATC	ACA	AGT	GAT	ATG	GCA	GAT	TAC	CAG	CAG	1697	
P	L	M	I	G	T	G	T	V	T	R	K	G	S	T	F	R	P	M	D	562	
CCC	CTC	ATG	ATT	GGC	ACC	GGG	ACA	GTC	ACG	AGG	AAG	GGC	TCC	ACC	TTC	CGG	CCC	ATG	GAC	1757	
T	D	A	E	E	A	G	V	S	T	D	A	G	G	H	Y	D	C	P	Q	582	
ACG	GAT	GCC	GAG	GAG	GCA	GGG	GTG	AGC	ACC	GAT	GCC	GGC	GGC	CAC	TAT	GAC	TGC	CCG	CAG	1817	
R	A	G	R	H	E	Y	A	L	P	L	A	P	P	E	P	E	Y	A	T	602	
CCG	GCC	GGC	CGC	CAC	GAG	TAC	GCG	CTG	CCC	CTG	GCG	CCC	CCG	GAG	CCC	GAG	TAC	GCC	ACG	1877	
P	I	V	E	R	H	V	L	R	A	H	T	F	S	A	Q	S	G	Y	R	622	
CCC	ATC	GTG	GAG	CGG	CAC	GTG	CTG	CGC	GCC	CAC	ACG	TTC	TCT	GCG	CAG	AGC	GGC	TAC	CGC	1937	

Fig. 10D

Fig. 10E

AAAACAAGCAAAGAAACACACCTCAGCAGCTGCCCGTTTCCTTAGTCTCCACTTCAGAGGGGGATGCCAAGAGGTCGG 2930
 CCCAGCTCCGGTGACCATGAAGGTGGCACAGGAATTACAGTGTGAATGGCTGTGTCAGATGTTTTTCGTACCTCAGATT 3009
 AAAATATTGCTGAGGTCAGACGCCACAAATTTTCATGACTTTCTTCAGAAGTAGCACATTTTCGTGACTTCCGCTGTCT 3088
 CTGAAAAACAAGTTATTTGGAACATGTTCAAGCAAGTCTGACCAAGTCTAAATCGAGCTTTTCTACTGACAT 3167
 GAACTGTTGGAAACTGATCTCAATTTTATAAGAAATGATTTTCCCTCAAGGAGCGCTGTAAATCCAGAACAAGTCCA 3246
 GACATCAGCTGTACCTCATGCTCAGTAGTTTATTTGAGTTTCTTTTGTGAGTTAACTATGGGAGATTTAACCTCTTT 3325
 TGCCAAAGAGGGAAGTGTGTGTTTTTTAATAGAAAAATATGGACCAAAAATTTTTTCCCTGAAGAATGTATTATAA 3404
 CCTATTGTGTGGTTATTACATCCTGTGAAATGTATATATGTTAAAAATAATGGGGGTGCTGGAAGGTCATGGCAGACT 3483
 AGCTGCTGGTTAGTGTGGAGGGGAAGTGGTTTACTTTGTAGAGTTTACATGGTTTATGCGCACACACTAATTGTAATAA 3562
 CTATGCCAAACCAAAATAAAAAAATAAAAAA

Fig. 10F

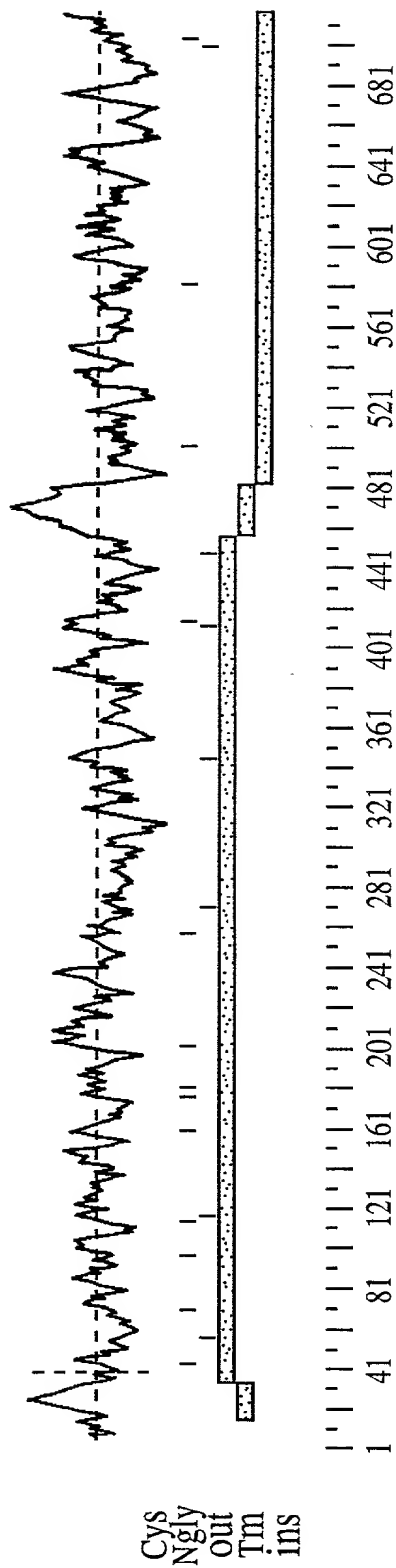


FIG. 10G

Letter "Q" Data

GTGGTCGCGCGAGGTGAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGC	79
CCCTGCGCTGCCACACCAAGCATTAGGCCACCAGGAAGACCCCATCTGTCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAG	158
M N W H M I I S G L I V V V	
GCCCCCTGCAGCTCCTTCATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG	14 220
L K V V G M T L F L L Y F P Q I F N K S	34
CTT AAA GTT GTT GGA ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT	280
N D G F T T T R S Y G T V S Q I F G S S	54
AAC GAT GGT TTC ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	340
S P S P N G F I T T R S Y G T V S Q I F G S S	62/361
TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC	74 400
W E F Y Q A R C F F L S T S E S S W N E	94
TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA	460
S R D F C K G K G S T L A I V N T P E K	114
AGC AGG GAC TTT TGC AAA GGA AAA GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA	520
L K F L Q D I T D A E K Y F I G L I Y H	134
CTG AAG TTT CTT CAG GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT	580

Fig. 11A

R E E K R W R R W I N N S V F N G N V T N 154
CGT GAA GAG AAA AGG TGG CGT TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC AAT 640

Q N Q N F N C A T I G L T K T F D A A S 174
CAG AAT CAG AAT TTC AAC TGT GCG ACC ATT GGC CTA ACA AAG ACA TTT GAT GCT GCA TCA 700

C D I S Y R R I C E K N A K * 188
TGT GAC ATC AGC TAC CGC AGG ATC TGT GAG AAG AAT GCC AAA TGA 745
TCACAGTTCCTGTGACAAGAACTATACTTGCAACTCTTTTGAATCCATACAGGTCGTCTGGCCAAATGATTTCTTTAC 824
TTACCTATCTGTCTACCAAGTAGCGTCTTGGCAATTTGGAAACTGAGCTTCTTCTTCTGCACTGGGGGACTGGATG 903
CTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCGGCTTCTGTAGTAC 982
TGAGCATTTCTGACTGATCAAAAAGGCTAGTCTGTTGACAGGTTTGTGTTTATTTTAGCCTCAGAGTATACCATACCTA 1061
CTAGGGAGTAACCTGTAGAGTGAGAAATATAAACATTAATTAGGGATTACCATGTTGAAAGAGGGATAAACATAGGTCC 1140
TGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCTCCTAACTCCACAAGCAGGGTAGCAGAGGCTCT 1219
CCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAATTGTTT 1298
ATGGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAAACCAGGCAGCCAAAGGAGC 1377
CAAAACACACTAGATTCTGTTCTTCAGCAAAAGCCCTGAAGAGACACTTAAGCTAAAAAATTCCTTGTCTGATTTCTGAA 1456
ACTCCATTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCTTGTCTGAAAGGTTTGTAGTA 1535
CCTGGCTGTATTTGTGTAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTCATCCCTTC 1614
AGTTCCTGGAGAAAGCCTGATACAGGCACAGCCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA 1693
GAACTGTCAGCCCGAAGAGTAGGAAAGAGAGAGGCTGCTCAGGGAAAACATTGGCTGGGGCAGCGAATAAGCAC 1772
ATAGTAAAAAGGGAACATCAGGGTCAAAATGGAATCACCTGAGACAGGAAACAGGGAGTTCAATTGGCCACACTGGAAG 1851
AAAGGCAAGAAAGAGGAACACAAGTCTTGGAGTACCTTGGCTGTTCTCCACACTCAAGACATCAGCTATACCTCTGCT 1930
TGGTGCTAAGAAAGAGAAAAGAGATGCCTTTTGTGTTTGTAGTAAAGAAATAATTAACCATTAAGGAAGACCATGTATAA 2009
AACTGATGGAAATAATAGTCAACCAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 2088

Fig. 11B

ACATGTCAATTGTATGTATACCAACAAGATTGTTGTAAATCATATTTTATTATCAACACATAAGTTCTGCTTCTGCATT 2167
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAA 2246
 CTTGCTTGAAGGGAATTACCAGAAGTAATTGTGTTTGAAGTGGGTGGAATTTGAATTAATATTAGTACCGGTGGAG 2325
 ATACAAGTTCTCTGACTGTGTTGGGAAGGATAAGTGCTACCGTTGAGAAGGAGAAAGGCTGAGTCTAGGTGGAGAA 2404
 AAATATCAACAGAACTCTAGCCAAAGCAAGCCCAAGAACTCAGACAAACAGAAAGGAATCCTAATCCTTCTGTTTGA 2483
 GAAGAGAGAACTGTAGTTGCTTCACTTCCCTATTTCAATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAAATGTAGACA 2562
 TCTAGTGATTTCTTTAGTAGACAGTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAATAAGGAGCCCA 2641
 ATGGCCCTGGGTGGAGTGGGAGTAGAGGAATATGTGGGATTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGA 2720
 TCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTA 2799
 GCAAGCCACTGAATTTGAGTTTTCACTTTGTCTAATATGCTGTGTGAATCAGTACAGTTTCTTACCCCTTCTTGGT 2878
 CTTAAATTTCTTACTGATAAAATGGGTAGTAATACCTATCTCAAAAAATTAATGCAATATAATAACATTCCTCTA 2957
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAAGTTGAGATCTTCATCCAAAGAGTAGCT 3036
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTTACTCATTTATAATATGGGAATA 3115
 AAAATTTGTGCAAGTCAGAGAAGGTGCTTAAAAAATGTTGTGGCCAAGCCACATGAGATCAAAAGACACACTTTTCATG 3194
 ACCTCAAAATGTGGGCCAGCCTAGGTCAGCCAAACCCCATCCAACTTAGACTCAGCAACAAATCCACCTGAGATCAG 3273
 CAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAAATAAAAACTTATCACTGTAAAAAAAATAAAAAAAA 3352
 GTCTCTCGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTAT 3431
 TGTTCATCCAGCAACCAGGATGATCTTGTAAAAACATTAAACAGATCTGTCAATCTTMAAAAAAAAAGCCATGA 3510
 AATTNTAGCAAGCCACTGAAATTTGAGTTTTCACCTTTGCTTCTAATAATGCTGTGTAATCAGANCAGKTTTCTTACCCT 3589
 TTCTTGGTCTTAATTTCCCTTACTGATAAAAATGGGTGWTAAATACCTATCTCAAAAAATTAATGACATATTARATAACA 3668
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG 3747
 AAGTAGCTTTTCAATTTGSTAGAAGCTTAAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATA 3826
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAAGACACAC 3905
 TTTTTCATGACCTCAAAATGTGGGCCAGCCTAGGTGAGCCAAACCCCATCCAACTTACCTTACGAAACAAATCCACCT 3984
 GAGATCAGCAGAGCCACCTAGATCAGCTGAAACTCTAAGCACAATAAAAACTTATCACTGTAAAAAAAATAAAAAA 4063
 AAAAAAAGAA 4074

Fig. 11C

GTGGT	CGCGCCGAGCTGTGAAGAAGAAACGTTGCTTGGCAAAAAGGAGCATATATTCTCAGGAGACGGGC	79
CCCTG	CCTGCCACACCAAGCATTAGGCCACCAGGAAGACCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAG	158
	M N W H M I I S G L I V V V	14
GCCCC	TGCAGCTCCTTCATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG	220
L K V	V G M T L F L L Y F P Q I F N K S	34
CTT AAA	GTT GTT GGA ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT	280
N D G	F T T R S Y G T V S Q I F G S S	54
AAC GAT	GGT TTC ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	340
S P S	P N G F I T T R S Y G T V S Q I F G S S	74
TCC CCA	AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	400
W E F	Y Q A R C F F L S T S E S S W N E	94
TGG GAA	TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA	460
S R D	F C K G S T L A I V N T P E K	114
AGC AGG	GAC TTT TGC AAA GGA AAA GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA	520
L K F	L Q D I T D A E K Y F I G L I Y H	134
CTG AAG	TTT CTT CAG GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT	580

Fig. 11D

R	E	E	K	R	W	R	W	I	N	N	S	V	F	N	G	K	Y	V	N	154
CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAG	TAC	GTG	AAC	640
M	P	Q	F	P	G	D	L	G	L	L	Q	K	T	K	P	E	I	A	G	174
ATG	CCA	CAG	TTT	CCT	GGG	GAT	CTT	GGT	TTG	CTT	CAA	AAG	ACC	AAA	CCT	GAG	ATT	GCT	GGG	700
F	T	L	E	*																178
TTC	ACC	CTG	GAA	TAG																715
CTCAAA	CGCTGACACT	CTGTTCTGCTCTTCTCCTTTCTTCCA	CCCATCTATTCCTATCTGTCTACCA	GTAGC	794															
GGTCC	TTGCCCATTTGGG	AAACTGAGCTTCTTTCTGCACTGGGG	ACTGGATGCTAGCCATCTCCAGGAGACAGGA	873																
TCAGT	TTTACGGAAACA	ACTCAGTTAGATAGAGATGAGTCCGCTTCTG	TAGTACTGAGCATTTCTGACTGATCAAAA	952																
AGCC	TAGTCTGTTGACAGGG	TTTGTATTTAGCCTCAGAGTATACCATACTACTAGG	AGTAACCTGTAGAGTGAG	1031																
AAATT	TATAAACATTTTAGGG	ATTACCATGGTGGAAGAGGGATAAACATAGG	TCTGTGACTTCGTCTCTGTTCTCAA	1110																
GGAA	CCCCCATTCACATG	CCCCCTCCTAACTCCACAAGCGAGGTAGCAGG	CTCTCCTCAGTCTGAACATAAGGCTTG	1189																
CCTT	GGGGAGGGCTCCTAG	TGCTGAGCTTGGAGCAGCACGGACAGCAT	TGTTATGGGAATGGAGAGGTTCTGGG	1268																
CAGGA	TAGGAACCTTCTTGAG	ACCCCTTTGAAGAAACAGGCAGCCAAAGGAG	CCAAACACACTAGATTCTGTCTT	1347																
TCAGC	AAAGCCCTGAAGAG	ACACTTAAGCTAAAAATTTCCCTTGTCATAT	TTCTGAACCTCCATTATAACATATGTA	1426																
CCTTT	GTAACCAAAATTTAG	GTAAGCAGGCTTCCCTTGCTCTGAAGGTTT	TGAGTACCTGGCTGTATTTGTGAGTAT	1505																
TTTAAA	ATTTTGGATAGTCT	CTTAGGCAACAATAATCACAAATATATTCAT	CCCTTCAGTTCTGGAGAAAGCCTGATAC	1584																
AGGCAC	AGCCTACTGACCC	CAAGAGCCTGGCACTGATTGGCATCACAT	TGATCTAGAACTGGTCCAGCCCGGAAGAG	1663																
TAGG	AAAAGAGAGGGCT	GCTCAGGGAAACATTTGGCTGGGGCACGGA	ATAAGCACATAGTAAAGGGAACATCAGGG	1742																
TCAA	ATGGAAATCACCT	GACAGGAAACAGGGAGTTCA	TTTGGCCACACTGGAAGAAAGCAAGAGG	1821																
GTCT	TGGAGTACCTGG	CTGTTCTCCACACTCACAAAGACATCAGC	TATACTCTGCTTGGTGCATAAGAAAGAG	1900																

Fig. 11E

GATGCCCTTTTGTGTTGAGTAAGAAATAATTAACCATATAAGGAAGACCATGTATAAAAATGATGGAAATAATAGTCACC 1979
AAAGTACAGCACATACCATTTTGTGCTAATAACAATGTAGCACAGTAATGACTGTACATGTCATTGTATGTATACCAA 2058
ACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCT 2137
CCTTAGCATGGCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGA 2216
AGTAATTGTGTTGAGATGGGTGGAATTTGGAATTATATTAGTAGCCGTGGAGATACAAGTTCTCTGACTGTGTTG 2295
GGAAGGATAAAGTGCTACCGTTGAGAAAGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2374
AAGGCAAGCCCGAAGCTCAGACAAACAGAAAAGGAATCCTAATCCTTCTGTTTTGAGAAGAGAGAACTGTAGTTGCTTC 2453
ACTTCCATTTCATGACAGAAATACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2532
GTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGAGTGGGGA 2611
GTAGATAGGGAATATGTGGATTGTTAAAGTTCATCATTTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGT 2690
GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTAGCAAGCCACTGAATTTGAGTTTT 2769
CACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAAT 2848
GGGTAGTAATAACCTATCTCAAAAAATTTATGCACATATTAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2927
TAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGCTAGAAAGCTTAAT 3006
GTAGGCAAGCCACTTCATTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 3085
GGTGCCTTAAAAATGTTGTGGCCAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGCCCAGCCTA 3164
GGTCAGCCAAACCCCATCCACCTTAGACTCAGAACAAATCCACCTGAGATCAGCAGAGCCACCTAGATCAGCTGA 3243
AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAATAAAAAAGTCTCTCGTATAGCAAAATCTAA 3322
CTGATGCAATCTCCATCTGCCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTATTGTTTCATCCAGCAACCAGGATGA 3401
TCCTTGTAAAAACATTAAACAGATTCTGTCAKCTTTMAAAAAAAAAGCCATGAAATNTAGCAAGCCACTGAAATTT 3480
GAGTTTTCACTTTGGTTTCTAATATGCTGTGAATCAGANCAGKTTTCTTACCCCTTTCTTGGTCTTAATTTCCTTACT 3559
GATAAAATGGGTWGTAAATACCTATCTCAAAAAATTTATGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3638
TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGSTAGA 3717

Fig. 11F

AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTCTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGT 3796
 CAGAGAAGGGTGCCCTTAAATAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC 3875
 CCAGCCTAGGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGA 3954
 TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 4018

Fig. 11G

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79
 AGCATTAGGCCACCCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGCCCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V L K V V G 19
 ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218

M T L F L L Y F P Q I F N K S N D G F T 39
 ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC 278

T T R S Y G T V C P K D W E F Y Q A R C 59
 ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 338

F F L S T S E S S W N E S R D F C K G K 79
 TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA 398

G S T L A I V N T P E K L K F L Q D I T 99
 GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT 458

Fig. 11H

D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	119
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	518
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	139
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	578
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	159
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	638
C	E	K	N	A	K	*														165
TGT	GAG	AAG	AAT	GCC	AAA	TGA														659
TCACAGT	TCCC	TGTGACA	GAAGAACTATAC	TTGCAACTCTTTT	TGAATCCATACAGGTCGTCTGGCCAAATGATTC	TTTAC														738
TTACCTAT	CTGTCTACCA	GAGCGGTCCTTGCCCATTTGGGAACTGAGCTTCTTCTTGCACTGGGGACTGGATG																		817
CTAGCCAT	CTCCAGGACACAGGATCAGTTTACGGAAACAAC	CTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC																		896
TGAGCAT	TTCTGACTGATCAAAAAGGCCTAGTCTGTTGACAGGGTTTGT	TTTATTTTAGCCCTCAGAGTATACCATACTA																		975
CTAGGGAG	TAACTGTAGAGTGAGAAATTATAAACATTTATAGGGATTACCATGGTGAAGAGGGATAAACATAGGTCC																			1054
TGTGACT	TCGTCTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAGCAGGGTAGCAGAGGCTCT																			1133
CCTCAGT	CTGAAC	TAGGCTTGGCCTTGGGAGGGCTCCTAGTGTGAGCTTGAGCAGCACGGACAGCAGCATTTGTTT																		1212
ATGGGAAT	GGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCCAGGCAGCCAAAGGAGC																			1291
CAAAACAC	ACTAGATTTCTGTCTTCAGCAAAAGCCCTGAAGAGACACTTAAGCTAAAATTCCTTGTCTATATTTCTGAA																			1370
ACTCCATT	TATAACATATGTAACTCCTTTGTAAACCAAAATTTAGTAAGCAGGCTTCTTGTCTCTGAAGGTTTGTAGTA																			1449
CCTGGCT	GTATTTGTGAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAAATAATCACAAATATATTCATCCCTTC																			1528
AGTTCTG	AGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA																			1607

Fig. 11I

GAACTGGTCCAGCCGCGAAGAGTAGGAAAAAGAGAAGGGCTGCTCAGGGAAACAATTGGCTGGGGCACGGAATAAGCAC 1686
 ATAGTAAAAAGGGAACATCAGGGTCAAATGGAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAG 1765
 AAAGGCAAGAAAGAGGAAACAAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCT 1844
 TGGTGCAATAAGAAAGAGAAAGAGATGCCTTTTGTGTTTGTAGTAAAGAAATAATTAAACCATAAGGAAGACCATGTATAA 1923
 AACTGATGGAATAATAGTACCAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 2002
 ACATGTCATTGTATGTATACCAAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTCTCTGCTTCTGCATT 2081
 CCTAGGTTTCATCATTTTTGGCTCCTTAGCATGGCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAA 2160
 CTTGCTTGAAAGGGAATTACCAGAAAGTAATTGTGTTTGAGATGGGTGGAATTTGGAATTAATATTAGTAGCCGGTGGAG 2239
 ATACAAAGTTCCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2318
 AAATATCAACAGAACTCTAGCCAAAGCAAGCCCAAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTTGA 2397
 GAAGAGAACTGTAGTTGCTTCACTTCCTATTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACA 2476
 TCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA 2555
 ATGGCCCTGGGGTGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAAGTTCATCATTTGGAGAGTTCCTGGA 2634
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTA 2713
 GCAAGCCACTGAATTGAGTTTTCACCTTTGTTTCTAATAATGCTGTGTAATCAGTACAGTTTCTTACCCTTTCTTGGT 2792
 CTTAATTTCCCTTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAAATTAATTGCACATATTAAATAACATTCCTCTA 2871
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT 2950
 TTTCAAATTTGCTAGAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCTCATTTATAATAATGGGAATA 3029
 AAAATTTGTGCAAGTCAGAGAAGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATG 3108
 ACCTCAAATGTGGGCCAGCCTAGGTCAGCCCAACCCCATCCAAACCTTAGACTCACGAAACAAATCCACCTGAGATCAG 3187
 CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAAAATAAAAAAATAAAAAA 3266
 GTCCTCGTATAGCAAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCCTTCTCCCTTTATTTGTCCTTTCGTGTAT 3345
 TGTTCATCCAGCAACCAGGATGATCTTTGTTAAACATTAACAGATTCTGTCAKCTTTMAAAAAATAAAAAAGCCATGA 3424
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCT 3503

Fig. 11J

TTCTTGGTCTTAATTCCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACA 3582
 TTCCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG 3661
 AAGTAGCTTTTCAATTGTGTAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTCTTACTCATTTATAATA 3740
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACAC 3819
 TTTTCATGACCTCAAATGTGGCCAGCCTAGGTAGCCCAACCCCATCCACCTTAGACTCACGAACAAATCCACCT 3898
 GAGATCAGCAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3977
 AAAAAAA 3985

Fig. 11K

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79
 AGCATTAGGCCACCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V V L K V V G 19
 ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218
 M T L F L L Y F P Q I F N K S N D G F T 39
 ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC 278
 T T R S Y G T V C P K D W E F Y Q A R C 59
 ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 338

Fig. 11L

[illegible]

Fig. 11M

CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCCTTTGCTCTGAAGGTTTTGAGTACCTGGCTGTATTTTGTGAGTATT 1419
 TTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTATCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1498
 AGGCACAGCCTACTGACCCCAAGAGCCTGGCAGTGGCATCACATTTGATCTAGAACTGTGTCCAGCCGCCGAAGAG 1577
 TAGGAAAAGAGAAGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1656
 TCAAAATGGAATCAACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAGAAAGCAAGAGGAAAGACAA 1735
 GTCCTGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATACTCTGCTTGGTGCAATAAGAAAGAGAAAAGA 1814
 GATGCCTTTTTGTGTTTGTAGTAAGAAATAATTAACCATAAGGAAGACCATGTATAAACTGATGGAAATAATAGTCACC 1893
 AAAGTACAGCACATACCATTTTGTGCTAATAACAATGTAGCACAGTAATGACTGTACATGTTCATTTGTATGTATACCAA 1972
 ACAAGATTGTTGTAATCATATTTTTTTATTACAACACTAAGTTCTGCTTCTGCAATTCCTAGGTTTCATCATTTTTTGGCT 2051
 CCTTAGCATGCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTGAGAACTTGCTTGAAGGGAATTACCAGA 2130
 AGTAAATTTGTGTTTGAGATGGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTG 2209
 GGAAAGGATAAGTGCTACCGTTGAGAAAGGAGAAAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2288
 AAGGCAAGCCCCAGAACTCAGACAAACAGAAAAGGAAATCCCTTCTGTTTTGAGAAAGAGAACTGTAGTTGCTTC 2367
 ACTTCCCTATTTTCATGACAGAAATAACTGCAAAATTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2446
 GTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAAGGAGCCCCAATGGCCTGGGTGGAGTGGGA 2525
 GTAGATAGGGAATATGTGGGATTGTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGATCCTTGCAAGCTTAGATAAATGT 2604
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAATTTAGCAAGCCACTGAATTTGAGTTTTT 2683
 CACTTTGTTTCTAAATATGCTGTGTAATCAGTACAGTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAAT 2762
 GGGGTAGTAATACCTATCTCAAAAAATATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2841
 TAGGAGAAGCAATTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGTAGCTTTTCAATTTGCTAGAAAGCTTAAT 2920
 GTAGGCAAGCCACTTCATTTTTCAGAACTTGTCTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 2999
 GGTGCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAGACACACTTTTCATGACCTCAAAATGTGGCCAGCCTA 3078
 GGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCTTAGATCAGCTGA 3157
 AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGTCTCTCGTATAGCAAAATCTAA 3236

Fig. 11N

CTGATGCAATCTCCATCTGGCCCTTCATCCTTCTCCCTTTATTGTGTCCTTTTCGTGTATTGTTCAATCCAGCAACCAGGATGA 3315
TCTTGTTAAACATTAACAGATTCTGTCAKCTTTMAAAAAAAGCCATGAAATNTAGCAAGCCACTGAATTT 3394
GAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCTTAATTTCTTACT 3473
GATAAAATGGGTGTGTAATACCTATCTCAAAAAATATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3552
TTAGACATTAGGAGAAGCATTTTGTGAGGATTTGAAGTTGAGATCTTCATCCAGAAAGTAGCTTTTCAATTTGSTAGA 3631
AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGT 3710
CAGAGAAGGTGTCCTTAAATAATGTTGTGGCCAAAGCCACATGAGATCAAGACACACTTTTCATGACCTCAAAATGTGGGC 3789
CCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGA 3868
TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAGAAAAAGAAAGAACCTTGCCCCG 3947
GGCGGCGGCC 3958

Fig. 110

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGAGCATATTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79
AGCATTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V V L K V V G 19
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218
M T L F L L Y F C P K D W E F Y Q A R C 39
ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 278
F F L S T S E S S W N E S R D F C K G K 59
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA 338

Fig. 11P

G	S	T	L	A	I	V	N	T	P	E	K	L	K	F	L	Q	D	I	T	79
GGA	TCC	ACA	TTG	GCA	ATT	GTC	AAC	ACG	CCA	GAG	AAA	CTG	AAG	TTT	CTT	CAG	GAC	ATA	ACT	398
D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	99
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	458
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	119
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	518
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	139
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	578
C	E	K	N	A	K	*														145
TGT	GAG	AAG	AAT	GCC	AAA	TGA														599
TCACAGT	TCCCTGTGACAA	GAAC	TATAC	TTGCA	ACTCTTTT	TGAATCC	ATACAGG	TCGTCTGGC	CAATGAT	CTTTTAC										678
TTACCTAT	CTGTCTAC	CAGTAG	CGGTCTT	GGCCCAT	TTGGGAA	AACTGAG	CTTCTTTCT	TCTGCA	CTGGGGAC	TGGATG										757
CTAGCCAT	CTCCAGGAG	ACAGGAT	CAGTTT	TACGGA	AACTCAG	TTAGTAT	AGATGAGG	TCCGCTT	CTGTAGTAC											836
TGAGCAT	TTCTGACT	GATCAAAA	AGGCTAG	CTGTGAC	AGGTTT	GTATTT	ATTTAG	CCCTCAG	AGTATAC	CATACTA										915
CTAGGGAG	TAACTGTAG	AGTGAGAA	ATTATA	AAACAT	TATTAG	GGATTACC	ATGGTGG	AAAGGG	ATAACATAG	GTCC										994
TGTGACT	TCGTCTCT	CTCAAGG	AAACCC	CAATTC	ACATG	CCCCCTC	CTAACTC	CAAGC	AGGGTAG	CAGAGG	CTCT									1073
CCTCAG	CTGAAC	TAAAGG	CTTGGG	GAGG	CTCCTAG	TGCTGAG	CTTGG	AGCAGC	ACGGAC	GACAGC	ATTGTTT									1152
ATGGGA	ATGGAG	AGGTCT	GGCAG	GATAGG	AACTTCT	TGGAG	ACCCCTT	TGAAG	AAACCA	GGCAGC	CAAGG	GAGC								1231

Fig. 11Q

CAAACACACTAGATTCTGTTCTTCAGCAAAAGCCCTGAAAGAGACACTTAAAGCTAAAAATTCCTTGTTCATATTTCTGAA 1310
 ACTCCATTATAACATATGTAACCTCTTGTAAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTA 1389
 CCTGGCTGATTTGTTGAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTCATCCCTTC 1468
 AGTCTGGAGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA 1547
 GAACTGTCCAGCCGCCGGAAGAGTAGAAAAAGAGAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCAC 1626
 ATAGTAAAAAGGGAACATCAGGGTCAATGGAAATCACCTGAGACAGGAAACACAGGAGTTTCATTTGGCCACACTGGAAG 1705
 AAAGGCAAGAAAGAGGAAAGACAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATACTCTGCT 1784
 TGGTGCAATAAGAAAGAGAAAGAGATGCCCTTTTGTGTTTGGTAAGAATAATTAAACCATAAAGGAAGACCATGTATAA 1863
 AACTGATGGAAATAATAGTCACCAAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 1942
 ACATGTCAATTGTATGTATACCAAAACAAGATTGTTGTAATCATATTTTATTATACAACACTAAAGTTCTGCTTCTGCATT 2021
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAA 2100
 CTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTGGATGGGTGGAATTTGGAATTATATATAGTAGCCGGTGGAG 2179
 ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2258
 AAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACACAGAAAGGAAATCCTAATCCTTCTGTTTGA 2337
 GAAAGAGAACTGTAGTTGCTTCACCTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAAGATCAGGAAATGTAGACA 2416
 TCTAGTGATTTCTTTAGTAGACAGTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA 2495
 ATGGCCTGGGTGGAGTGGGAGTAGATAGGGAATATGTGGATTTGGTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGA 2574
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTTA 2653
 GCAAGCCACTGAATTTGAGTTTTCACCTTTGTTTCTAATATGCTGTGTAATCAGTACAGTTTCTTACCTTCTCTGGT 2732
 CTTAATTTCCCTTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAATTTATTGCACATATTAAATAACATTCCTCTA 2811
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT 2890
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGAATA 2969
 AAAATTTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACTTTTTCATG 3048
 ACCTCAAATGTGGGCCAGCCTAGGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAG 3127

Fig. 11R

CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3206
GTCTCTCGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTAT 3285
TGTTCAATCCAGCAACCAGGATGATCTTGTTAAACATTAACAGATTCTGTCA YKCTTMAAAAAAAGCCATGA 3364
AATTNTAGCAAGCCACTGAAATTTGAGTTTTCACCTTGGTTTCTAATATGCTGTGAA TCAGANCAGKTTTCTTACCCCT 3443
TTCCTGGTCTTAATTCCTTACTGATAAAATGGGTWGTAAATACCTATCTCAAAAAATATTGCACATATTARATAACA 3522
TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCATCCAAG 3601
AAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTACTCATTTATAATA 3680
TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAAGACACAC 3759
TTTTTCATGACCTCAAAATGTGGGCCCAGCCTAGGTGAGCCCAACCCCATCCAACTTAGACTCACGAAACAAATCCACCT 3838
GAGATCAGCAGAGCCACCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3917
AAAAAAA 3925

Fig. 11S

GAGACTGTGAAGAAGAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCTGCCCTGCCACACCA 79
 AGCATTAGGCCACCCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V V L K V V G 19
 ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218

M T L F L L Y F C P K D W E F Y Q A R C 39
 ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 278

F F L S T S E S S W N E S R D F C K G K 59
 TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA 338

G S T L A I V N T P E K L K F L Q D I T 79
 GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT 398

D A E K Y F I G L I Y H R E E K R W R W 99
 GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT GAA GAG AAA AGG TGG CGT TGG 458

I N N S V F N G K Y V N M P Q F P G D L 119
 ATC AAC AAC TCT GTG TTC AAT GGC AAG TAC GTG AAC ATG CCA CAG TTT CCT GGG GAT CTT 518

G L L Q K T K P E I A G F T L E * 135
 GGT TTG CTT CAA AAG ACC AAA CCT GAG ATT GCT GGG TTC ACC CTG GAA TAG 569

78/361

Fig. 11T

CTCAAACGCTGACACTTGACTCTGTTCTGCTCTTCTCCTTTCTTCCAACCCATCTATTTCCCTATCTGTCTACCACTAGC 648
GGTCCCTTGCCCATTTGGGAAACTGAGCTTCTTTCTTCTGCACCTGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA 727
TCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGATCAAAA 806
AGCCCTAGTCTGTTGACAGGGTTTGTTTATTTTAGCCTCAGAGTATACCATACTACTAGGAGTAACCTGTAGAGTGAG 885
AAATTATAAACATTATTTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTCTCTCAA 964
GGAAACCCCATTCACATGCCCTCCTAACTCCACAAGCGAGGTAGCAGAGGCTCTCCTCAGTCTGAACATAAGGCTTGG 1043
CCTTGGGGAGGGCTCCTAGTGTGAGCTTGAGCGACGCGACAGCAATGTTTATGGGAATGGAGAGAGGTCCTGGG 1122
CAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAAGGAGCCAAACACACTAGATTTCTGTCT 1201
TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCTATATTTCTGAAACTCCATTATAACATATGTAAC 1280
CCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCCCTTGTCTGAAGGTTTTGAGTACCTGGCTGTATTTGTTGAGTATT 1359
TTTAAAAATTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTTCATCCCTTCAGTTCCTGGAGAAAAGCCTGATACC 1438
AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTTAGTCTAGAACTGGTCCAGCCGCCGAAGAG 1517
TAGGAAAAGAGAAAGGCTGCTCAGGGAAACATTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1596
TCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTCAATTTGGCCACACTGGAAAGAAAGCAAGAGAAAGACAA 1675
GTCTTGGAGTACCCCTGGCTGTCTCCACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGAGAAAAGA 1754
GATGCCTTTTTGTTGAGTAAGAAATAATTAAACCATAAGGAAGACCATGTATAAAACTGATGGAATAATAGTCACC 1833
AAAGTACAGCACATACCAATTTGTGTCTAATAACAATGTAGCACAGTAATGACTGTACATGTCAATGTATGTATACCAA 1912
ACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCT 1991
CCTTAGCATGGCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAAGAACTTGCTTGAAGGGAATTACCAGA 2070
AGTAATTTGTGTTTGAGATGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAGATACAAATTCTCTGACTGTGTG 2149
GGAAAGGATAAGTGCTACCGTTGAGAAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2228
AAGGCAAGCCCCAGAACTCAGACAACAGAAAAGGAAATCCTAATCCTTCTGTTTGGAGAAAGAGAACTGTAGTTGCTTC 2307
ACTTCCATTTTCATGACAGAATAACTGCAAAATTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2386

Fig. 11U

GTTTAATTTCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCAATGGCCCTGGGTGGAGTGGGGA 2465
 GTAGATAGGGAATATGTGGGATTTGGTTAAGTTCATCATTTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGT 2544
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAATTAGCAAGCCACTGAATTTGAGTTT 2623
 CACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTCTTACCCCTTCTTGGTCTTAAATTTCCTTACTGATAAAAT 2702
 GGGTAGTAATACCTATCTCAAAAAATATTGCACATATTAAATAACATTCCCTCTATGTATCTCAATGGCATTAGACAT 2781
 TAGGAGAAGCAATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAAAGTAGCTTTTCAATTTGCTAGAAAGCTTAAT 2860
 GTAGGCAAGCCACTTCATTTTCAGAACTTGTCTACTTATAATATGGGAATAAAAATTTGTGCAAGTCAGAGAAG 2939
 GGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGCCAGCCTA 3018
 GGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGA 3097
 AACTCTAAGCACAAAAATAAAAACTTATCACCTGTAAAAAAGGCAATGCTCTCGTATAGCAAAAATCTAA 3176
 CTGATGCAATCTCCATCTGGCCCTTCATCCTTCTCCCTTTATTGTCTTTCGTGTAATGTTTCATCCAGCAACCAGGATGA 3255
 TCTTGTAAAAACATTAAACAGATTCTGTCAKCTTMAAAAAAAGGCAATGAAATNTAGCAAGCCACTGAATTT 3334
 GAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCCTTTCTTGGTCTTAAATTTCCCTTACT 3413
 GATAAAATGGGTGTAATACCTATCTCAAAAAATATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3492
 TTAGACATTAGGAGAAGCAATTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGSTAGA 3571
 AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGT 3650
 CAGAGAAGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC 3729
 CCAGCCTAGGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3808
 TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAGGCAATGAAAGCAACCTGCCCCG 3887
 GCGGGCGGCCCC 3898

Fig. 11V

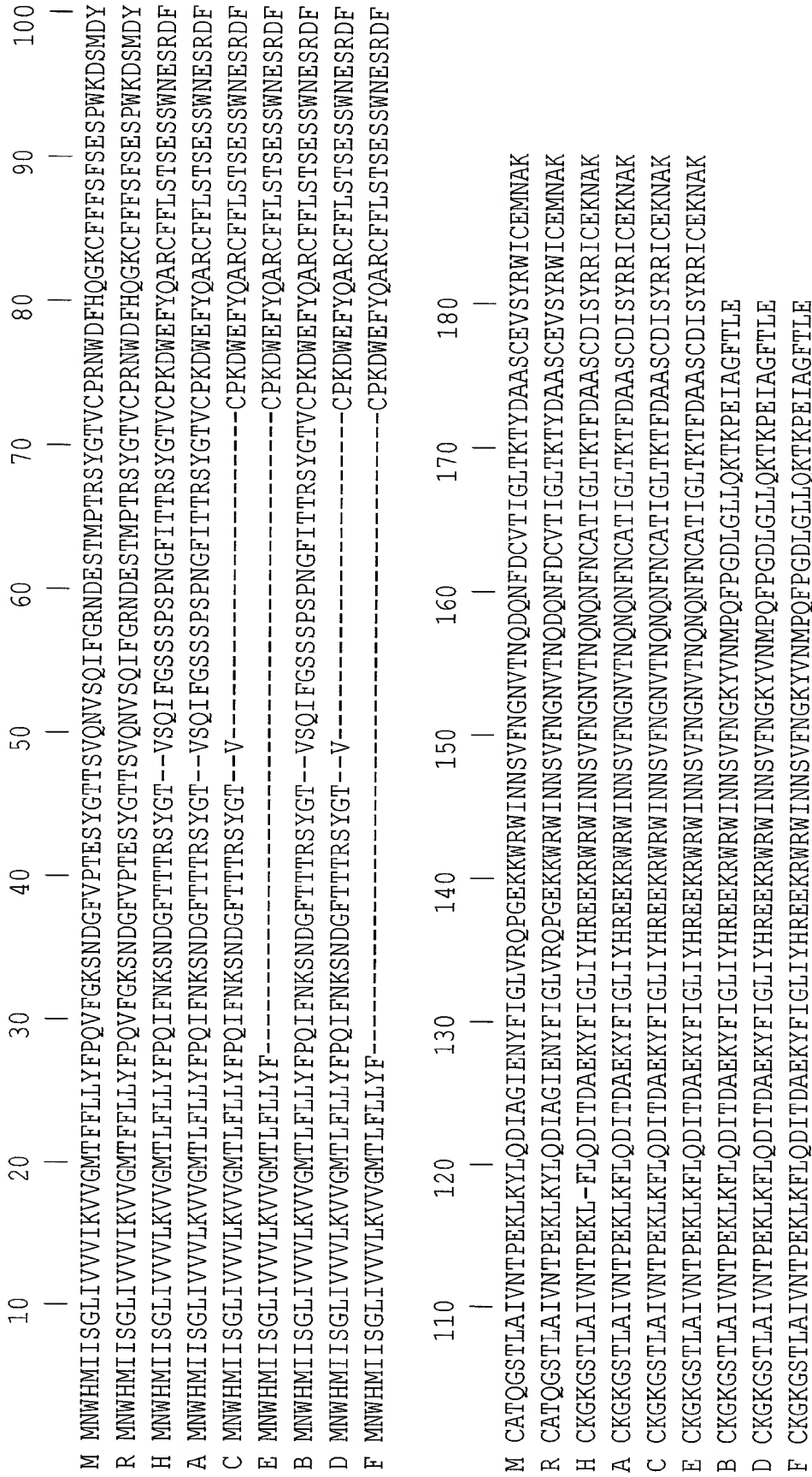


Fig. 11W

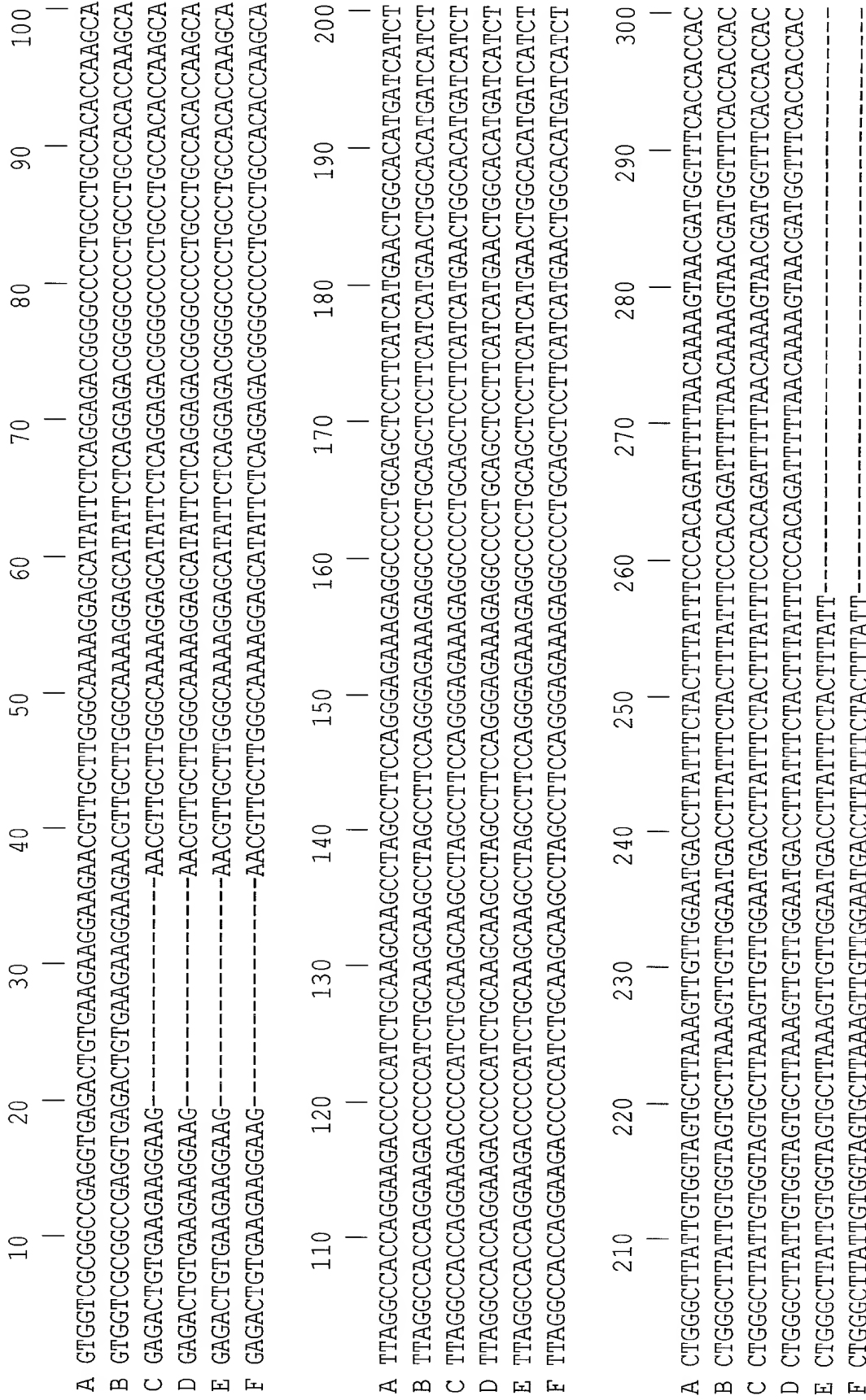


Fig. 11X-1

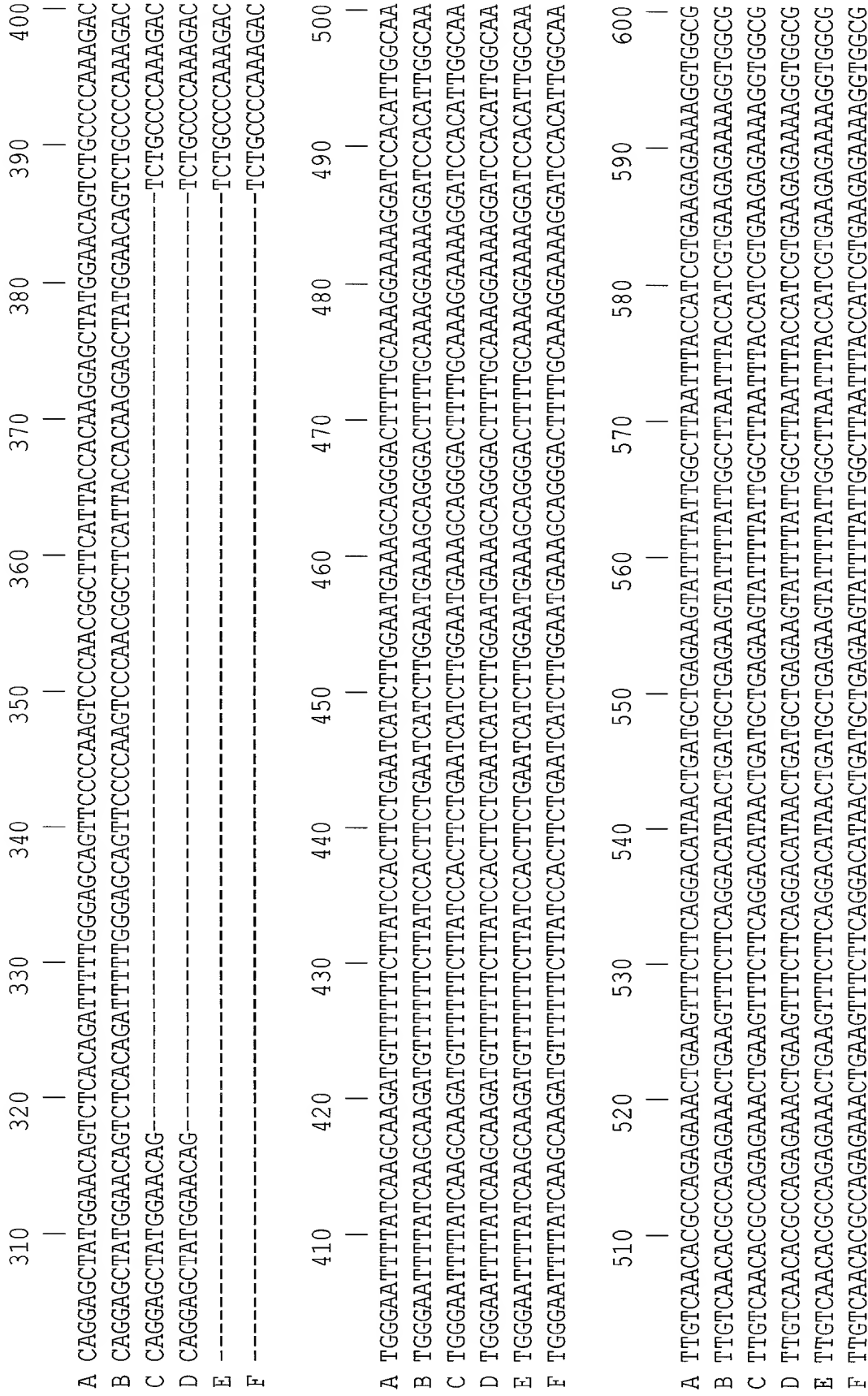


Fig. 11X-2

	610	620	630	640	650	660	670	680	690	700
A	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAATGTTACCA	ATCAGAATCAGA	ATTCAGAAATTC	ACACTGTGCG	ACCATTGGCC	TAAACAAGAC	ATTTGATGCTG	CAATCA
B	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAAGTACGTGA	ACATGCCACAGT	TTCCCTGGGGAT	CTTGGTTGCT	TTCAAAAGAC	CAAAACCTG	AGATTGCT	TGGG
C	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAATGTTACCA	ATCAGAATCAGA	ATTCAGAAATTC	ACACTGTGCG	ACCATTGGCC	TAAACAAGAC	ATTTGATGCTG	CAATCA
D	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAAGTACGTGA	ACATGCCACAGT	TTCCCTGGGGAT	CTTGGTTGCT	TTCAAAAGAC	CAAAACCTG	AGATTGCT	TGGG
E	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAATGTTACCA	ATCAGAATCAGA	ATTCAGAAATTC	ACACTGTGCG	ACCATTGGCC	TAAACAAGAC	ATTTGATGCTG	CAATCA
F	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAAGTACGTGA	ACATGCCACAGT	TTCCCTGGGGAT	CTTGGTTGCT	TTCAAAAGAC	CAAAACCTG	AGATTGCT	TGGG

	710	720	730	740	750	760	770	780	790	800
A	TGTGACATCAG	TACCGCAGGAT	CTGTGAGAA	GAATGCCAAATG	ATCATCAGAT	CCCTGTGACA	GAAGAACTAT	ACTTGCAACT	CTTTTGAAT	CCATACAGG
B	TTACCCCTGGA	ATAGCTCAAA	CGTGACACT	TCTGTTCTG	CTTCTCCCT	TTCTCCAA	ACCCATCTAT	TC-----		
C	TGTGACATCAG	TACCGCAGGAT	CTGTGAGAA	GAATGCCAAATG	ATCATCAGAT	CCCTGTGACA	GAAGAACTAT	ACTTGCAACT	CTTTTGAAT	CCATACAGG
D	TTACCCCTGGA	ATAGCTCAAA	CGTGACACT	TCTGTTCTG	CTTCTCCCT	TTCTCCAA	ACCCATCTAT	TC-----		
E	TGTGACATCAG	TACCGCAGGAT	CTGTGAGAA	GAATGCCAAATG	ATCATCAGAT	CCCTGTGACA	GAAGAACTAT	ACTTGCAACT	CTTTTGAAT	CCATACAGG
F	TTACCCCTGGA	ATAGCTCAAA	CGTGACACT	TGTGTTCTG	CTTCTCCCT	TTCTCCAA	ACCCATCTAT	TC-----		

	810	820	830	840	850	860	870	880	890	900
A	TCGCTGGCCAA	TGATCTTTTACT	TACCTATCTGT	CTACCAAGTAG	CGGTCCCTG	CCCCATTTGGG	AAACTGAGCT	TTCTTCTG	CACTGGGG	ACTTGG
B	-----									
C	TCGCTGGCCAA	TGATCTTTTACT	TACCTATCTGT	CTACCAAGTAG	CGGTCCCTG	CCCCATTTGGG	AAACTGAGCT	TTCTTCTG	CACTGGGG	ACTTGG
D	-----									
E	TCGCTGGCCAA	TGATCTTTTACT	TACCTATCTGT	CTACCAAGTAG	CGGTCCCTG	CCCCATTTGGG	AAACTGAGCT	TTCTTCTG	CACTGGGG	ACTTGG
F	-----									

Fig. 11X-3

Figure 11X-4

	910	920	930	940	950	960	970	980	990	1000
A	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT									
B	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT									
C	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT									
D	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT									
E	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT									
F	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT									
	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
A	CAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTGTTATTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACGTAGAGTGAGAAATTATAAACATTAT									
B	CAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTGTTATTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACGTAGAGTGAGAAATTATAAACATTAT									
C	CAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTGTTATTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACGTAGAGTGAGAAATTATAAACATTAT									
D	CAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTGTTATTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACGTAGAGTGAGAAATTATAAACATTAT									
E	CAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTGTTATTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACGTAGAGTGAGAAATTATAAACATTAT									
F	CAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTGTTATTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACGTAGAGTGAGAAATTATAAACATTAT									
	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
A	TTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG									
B	TTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG									
C	TTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG									
D	TTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG									
E	TTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG									
F	TTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG									

Fig. 11X-4



Fig. 11X-5

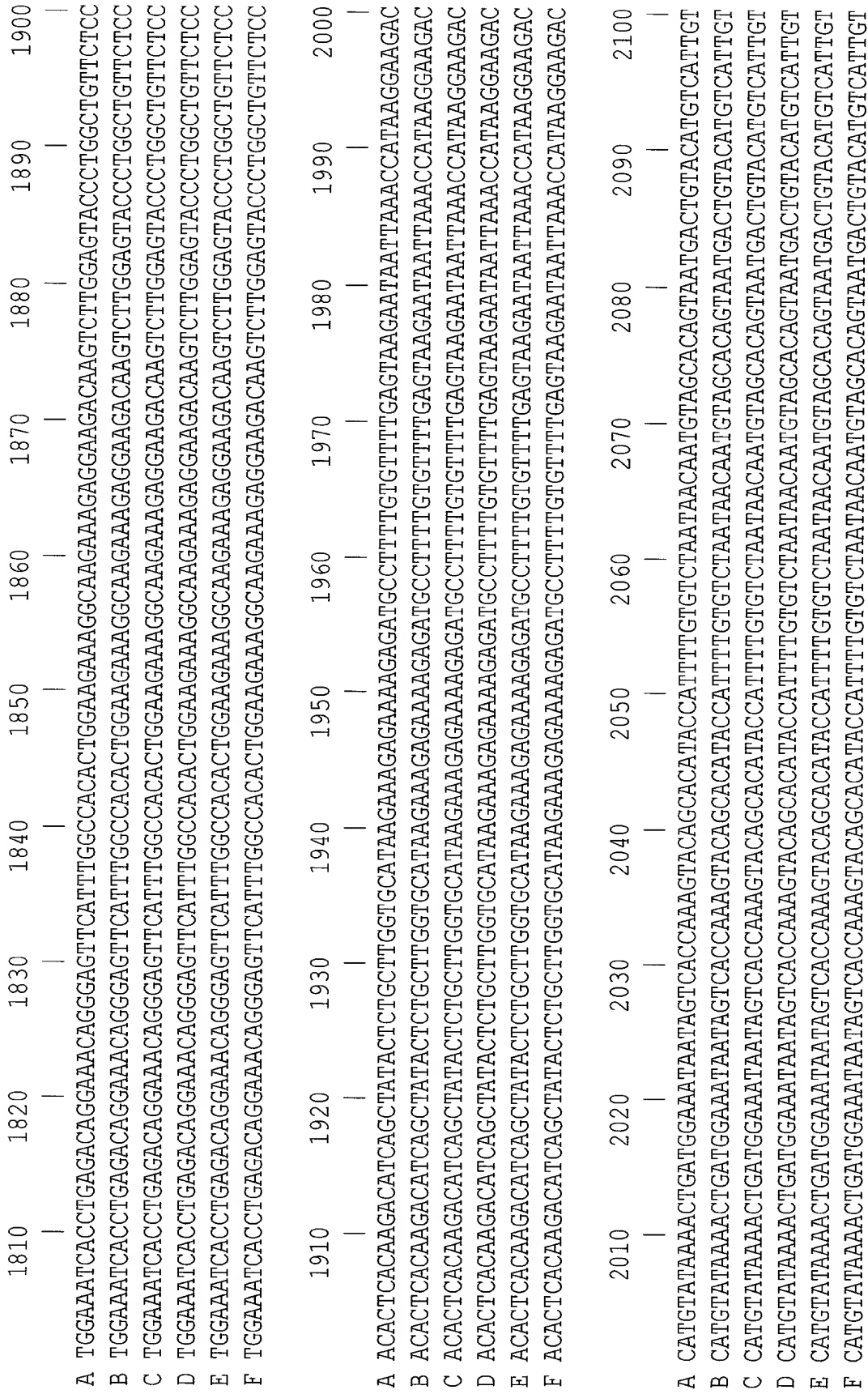


Fig. 11X-7

“let’s be free”

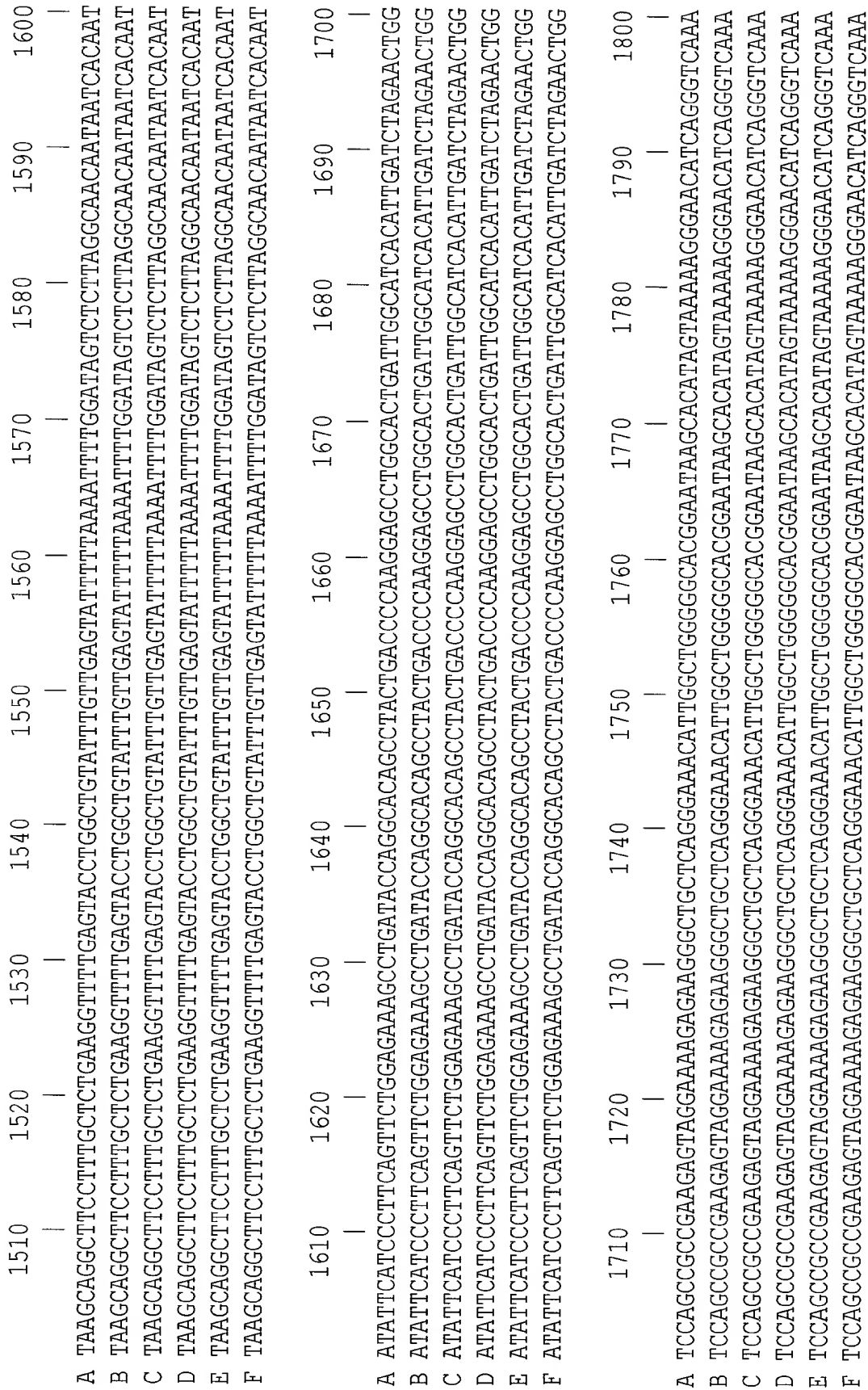


Fig. 11X-6

2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
A	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
B	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
C	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
D	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
E	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
F	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
A	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGAAATTT								
B	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGAAATTT								
C	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGAAATTT								
D	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGAAATTT								
E	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGAAATTT								
F	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGAAATTT								
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
A	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
B	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
C	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
D	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
E	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
F	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								

Fig. 11X-8

Figure 11X-9

	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	
A	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
B	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
C	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
D	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
E	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
F	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	
A	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA										
B	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA										
C	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA										
D	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA										
E	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA										
F	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA										
	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	
A	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA										
B	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA										
C	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA										
D	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA										
E	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA										
F	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA										

Fig. 11X-9

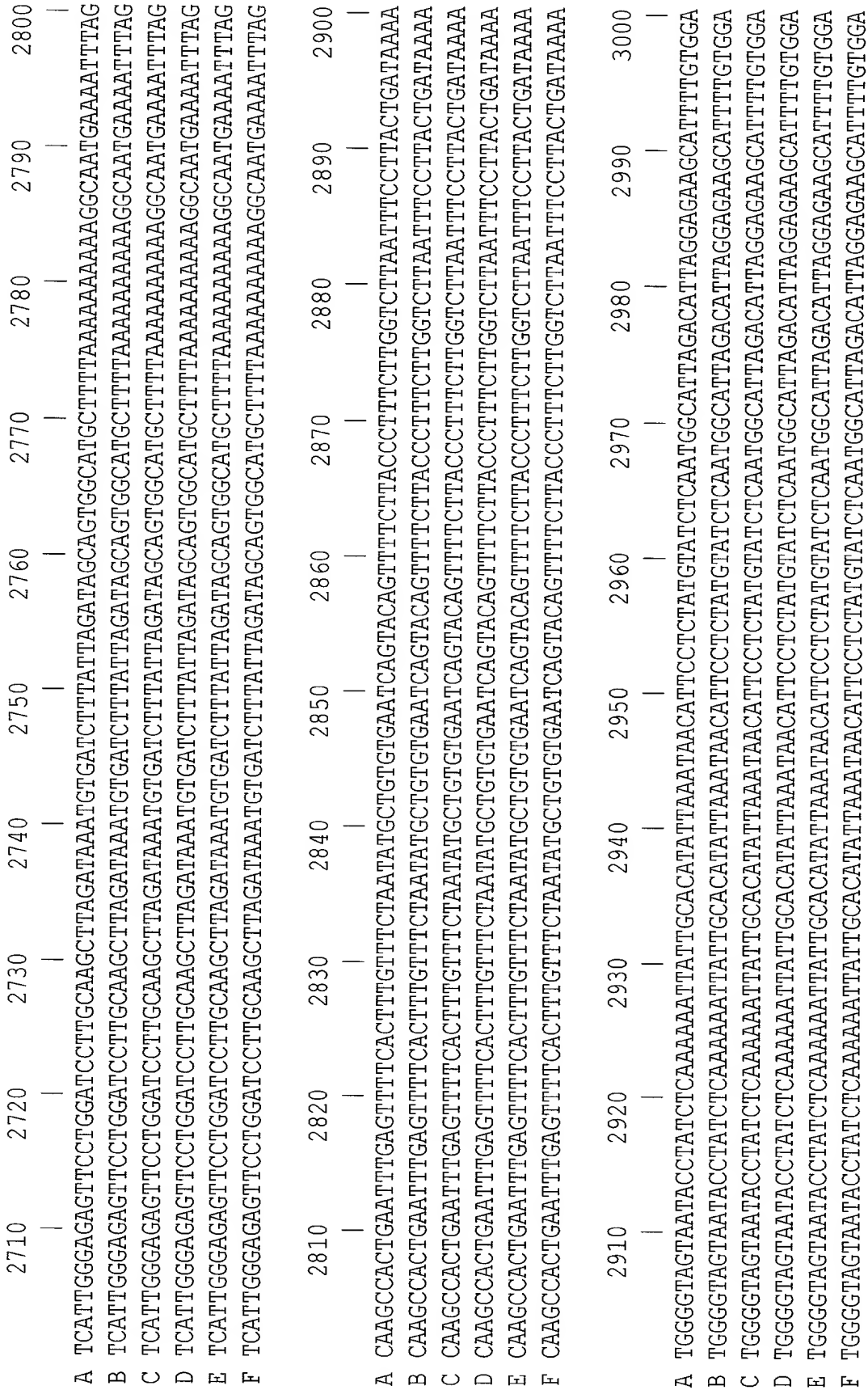


Fig. 11X-10

	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
A	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
B	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
C	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
D	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
E	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
F	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
A	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTGCCT	TAAAAATGTTGTGGCCAAGCCACAT	GAGATCAAAAGACACACTTT	TCATGACCTCA					
B	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTGCCT	TAAAAATGTTGTGGCCAAGCCACAT	GAGATCAAAAGACACACTTT	TCATGACCTCA					
C	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTGCCT	TAAAAATGTTGTGGCCAAGCCACAT	GAGATCAAAAGACACACTTT	TCATGACCTCA					
D	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTGCCT	TAAAAATGTTGTGGCCAAGCCACAT	GAGATCAAAAGACACACTTT	TCATGACCTCA					
E	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTGCCT	TAAAAATGTTGTGGCCAAGCCACAT	GAGATCAAAAGACACACTTT	TCATGACCTCA					
F	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTGCCT	TAAAAATGTTGTGGCCAAGCCACAT	GAGATCAAAAGACACACTTT	TCATGACCTCA					
	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
A	AATGTGGCCAGCCTAGGTCAG	CCAAACCCCATCCAACCCCTTAG	ACTCACGAACAATA	CCACCTGAGATCAGCAGAGCC	ACCCCTAGATCAGCTGAA	AACT				
B	AATGTGGCCAGCCTAGGTCAG	CCAAACCCCATCCAACCCCTTAG	ACTCACGAACAATA	CCACCTGAGATCAGCAGAGCC	ACCCCTAGATCAGCTGAA	AACT				
C	AATGTGGCCAGCCTAGGTCAG	CCAAACCCCATCCAACCCCTTAG	ACTCACGAACAATA	CCACCTGAGATCAGCAGAGCC	ACCCCTAGATCAGCTGAA	AACT				
D	AATGTGGCCAGCCTAGGTCAG	CCAAACCCCATCCAACCCCTTAG	ACTCACGAACAATA	CCACCTGAGATCAGCAGAGCC	ACCCCTAGATCAGCTGAA	AACT				
E	AATGTGGCCAGCCTAGGTCAG	CCAAACCCCATCCAACCCCTTAG	ACTCACGAACAATA	CCACCTGAGATCAGCAGAGCC	ACCCCTAGATCAGCTGAA	AACT				
F	AATGTGGCCAGCCTAGGTCAG	CCAAACCCCATCCAACCCCTTAG	ACTCACGAACAATA	CCACCTGAGATCAGCAGAGCC	ACCCCTAGATCAGCTGAA	AACT				

Fig. 11X-11

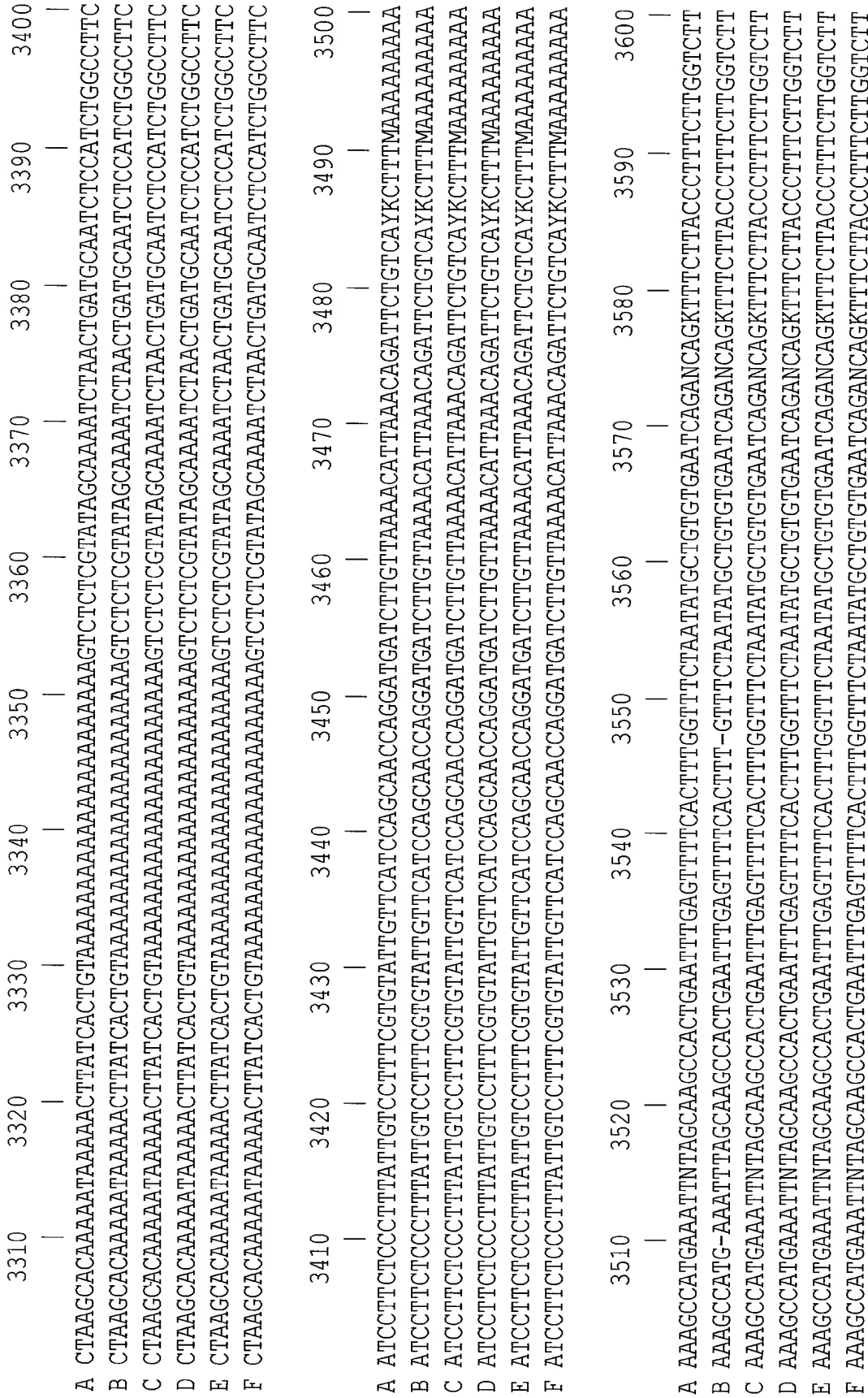


Fig. 11X-12

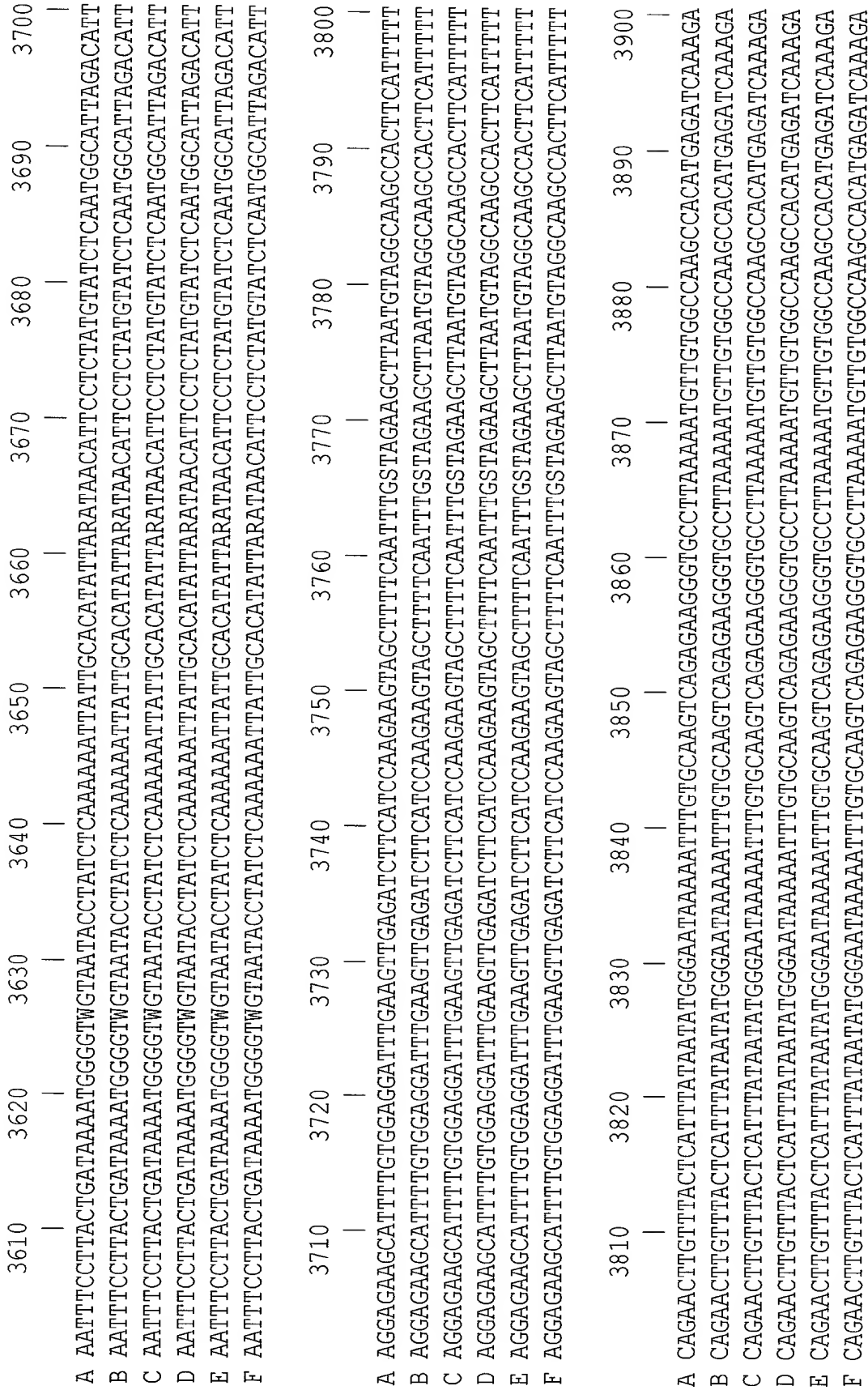


Fig. 11X-13

[illegible][illegible]

Fig. 11X-14

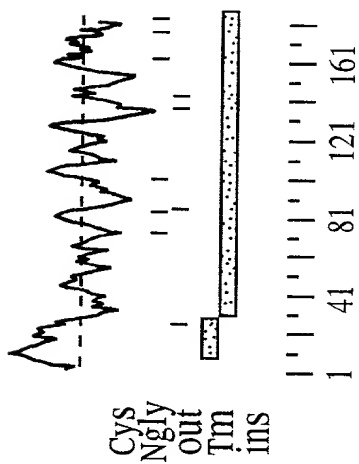


FIG. 11Y-1

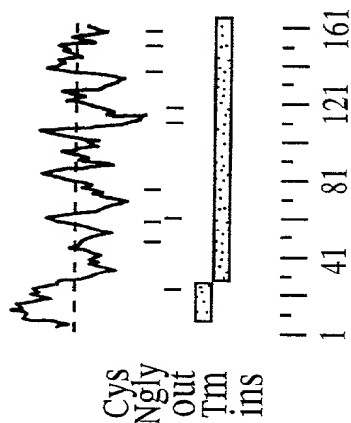


FIG. 11Y-3

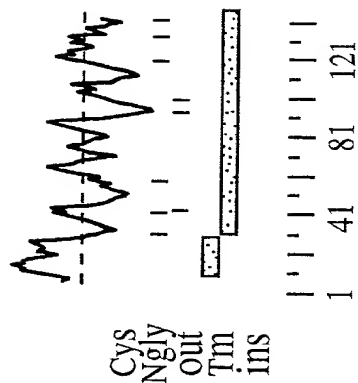


FIG. 11Y-5

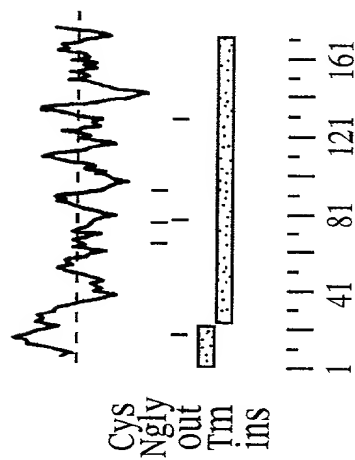


FIG. 11Y-2

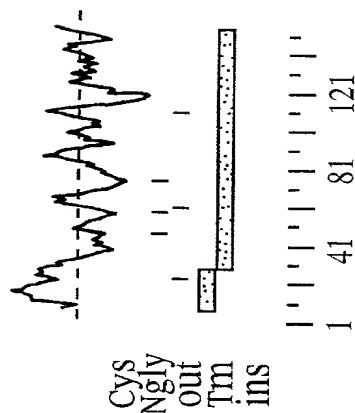


FIG. 11Y-4

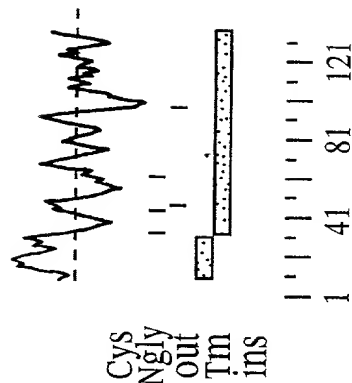


FIG. 11Y-6

GTCGACCCAC	CGGTCCGGTT	TGCTTGGAGA	TGCTGCTAAA	ACAGAGAGGC	TGTGAACAAG	60
GACATTACCG	AGCAGGAGCA	TACATTTCAGA	AGACAAGGAG	CCCTGCTCGC	TGCACCCGAAT	120
ATCTTATCAA	AAAGACTCCT	ATCTGTATGC	CAACCCAGAC	TTCCAGAAAG	AGATCAGATC	180
CCTGAATCCC	CATCATC	ATG AAC	TGG CAC	ATC ATC	TCG GGG	CTT ATC
	Met Asn	Trp His	Met Ile	Ile Ser	Gly Leu	Ile
	1	5	10			
GTA GTA	GTG ATC	AAA GTT	GTT GGA	ATG ACC	TTT TTT	CTG TAT
Val Val	Val Ile	Lys Val	Val Gly	Met Thr	Phe Phe	Leu Tyr
	15	20	25			
CCA CAG	GTT TTT	GGC AAA	AGT AAT	GAT GGC	TTC GTC	CCC ACG
Pro Gln	Val Phe	Gly Lys	Ser Asn	Asp Gly	Phe Val	Pro Thr
	30	35	40			
TAC GGA	ACC ACT	AGT GTG	CAG AAT	GTC TCA	CAG ATC	TTT GGG
Tyr Gly	Thr Thr	Ser Val	Gln Asn	Val Ser	Gln Ile	Phe Gly
	45	50	55			
GAC GAA	AGT ACC	ATG CCT	ACA AGG	AGC TAT	GGA ACA	GTC TGT
Asp Glu	Ser Thr	Met Pro	Thr Arg	Ser Tyr	Gly Thr	Val Cys
	60	65	70			
AAC TGG	GAT TTT	CAC CAA	GGA AAA	TGC TTT	TTC TTC	TCC TTC
Asn Trp	Asp Phe	His Gln	Gly Lys	Cys Phe	Phe Ser	Phe Ser
		80		85		90

Fig. 11Z-1

TCA CCT TGG AAA GAC AGC ATG GAT TAT TGT GCA ACA CAA GGA TCC ACA	518
Ser Pro Trp Lys Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr	95 100 105
CTG GCA ATT GTC AAC ACT CCA GAG AAA CTG AAG TAT CTT CAG GAC ATA	566
Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Lys Tyr Leu Gln Asp Ile	110 115 120
GCT GGT ATT GAG AAT TAC TTT ATT GGT TTG GTA CGT CAG CCT GGA GAG	614
Ala Gly Ile Glu Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu	125 130 135
AAA AAG TGG CGC TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC	662
Lys Lys Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr	140 145 150 155
AAT CAG GAC CAG AAC TTC GAC TGT GTC ACT ATA GGT CTG ACG AAG ACA	710
Asn Gln Asp Gln Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr	160 165 170
TAT GAT GCT GCA TCA TGT GAA GTC AGC TAT CGC TGG ATC TGC GAA ATG	758
Tyr Asp Ala Ala Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met	175 180 185

Fig. 11Z-2

AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT TACAGAGCTA	807
Asn Ala Lys	
190	
GCAAAGGAGA TTAGTTGTGA CTGAAACCAG CCCAGGAAAT ATAGAGCATC AAAGACTGTG	867
CCCATCTTCC ATAGGTGGAG TTCCCTATTG AATCCTCAAA GTCAATTTGT TACTCCACAA	927
ACATCTTCAC ATAGTAAAC TCCCTTTCTG ACCAAGTATT CCCTAAGACC ACACTTCCTG	987
TGAGAGGGGA CTGGATTCTA GTTATCTGCA GACAGAGCCA GGATTCTGGA GATGAAATCA	1047
ATATGGAAAT GCAGTCTGTT TCTGTAGAGC TGAGCCCTTTT AACTAATCAG TAGGGTTTGT	1107
TCTGTTGTCA GAACTGTTTG ATCCTTAGAG AACATGCCCA CGCCACTGAG GAGAAACTGC	1167
TCGTGGAACA GATATGAGAA CTGTTAGGAA GCACTATGGG CAGAAGAATA TAAACTTGGC	1227
TTCACAAACAT CCCCCATTCC AGAAAGCCCTC CCATTCCCAT ACAACATCGT AGAAGCAGAG	1287
GTCCCTTCTGA ATTGGGGAAG GACCTCTACA GCTCGACTTG GTACTGAACA AATATTGAGG	1347
GAATGAAGAA AGTTCCTGAAT AGGACAGAGA TAAACAAGGA GGAGAAAGGAA AGAGATAGGA	1407
AGAAAGGAGA AGTGGGAAGG AGGGGAAAA GGAATGATGG GCAGGAGAAA AAGAGACAGG	1467
AGCAGCCAGG AAAAACACTC AAGCTAAATT TTTTTCAGGT TTTGGATAAA ATCTATTGTG	1527
ACATAAATAA TATCTTTTCA TTAGAAGAGA AAAGGCAAAA TTGGGGACAA ATGGGCACCA	1587
TGAGAGATGA AGCAGAGGTT AATTGTATCA CAAGGAAAAG AAGCAGGAA TGAGGTTGAA	1647
AACTTTTTGG ATACCTTGGC TGTTATCTCA AGAAGGTACA AGCTGCATAA AGTATAGGAG	1707
AAAAGAGATG TGCTGGTTGT TTTAAGTAGC AAAAATTAAA CTACAGAGAA GCCTATAGAA	1767
AGCTAAAGGA ATTAAAAACCA TCCAAATAATC AATTCATTAT TTTCAACTAA TAGCAATATG	1827
TATGTGCATT ACTAGTCAAA ATAAATTGTG AATTCTGTTA TTATAAAAAA AAAAAAAAAG	1887
GGCGGCCGC	1896

Fig. 11Z-3

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MI289 ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTGATCAAAGTTGTTGGAATG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ATGAACTGGCACATGATCATCTCGGGGCTTATTTGGTAGTGCTTAAAGTTGTTGGAATG 60

MI289 ACCTTTTCTGCTGTAATTTCCACAGGTTTTTTGGCAAAAGTAATGATGGCTTCGTCCCC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCTTATTTCTACTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACC 120

MI289 ACGGAGAGCTACGGAACCACTAGTGTGCAGAAATGCTCACAGATCTTTGGGAGAAATGAC 180
      || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCAGGAGCTATGGAACA-----GTCTCACAGATTTTGGGAGCAGTTCCTCCCAAGTCCC 174

MI289 GAAAGTACCATGCCCTACAAGGAGCTATGGAACAGTCTGTCCCAGAAACTGGGATTTTCAC 240
      | | ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 AACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGTCCCCCAAGACTGGGAAATTTTAT 234

MI289 CAAGGAAAATGCTTTTCTCTCCTTCTCCGAATCACCTTGAAAGACAGCATGGATTAT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 CAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTT 294

```

Fig. 11Z-4

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MI289 ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG 60

MI289 ACCTTTTTCTGCTGTATTTCCCCACAGGTTTTTTGGCAAAAGTAATGATGGCTTCGTCCCC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCTTATTTCTACTTTATTTCCCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACC 120

MI289 ACGGAGAGCTACGGAACCACTAGTGTGCAGAAATGTCTCACAGATCTTTGGGAGAAATGAC 180
      || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCAGGAGCTATGGAACA-----GTCTCACAGATTTTGGGAGCAGTTCCCCCAAGTCCC 174

MI289 GAAAGTACCATGCCCTACAAGGAGCTATGGAACAGTCTGTCCCAGAAACTGGGATTTTCAC 240
      | | ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 AACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCCAAGACTGGGAATTTTAT 234

MI289 CAAGGAAAATGCTTTTCTCTCCTTCTCCGAATCACCTTGAAAGACAGCATGGATTAT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 CAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTT 294

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Fig. 11Z-4

Fig. 11Z-5

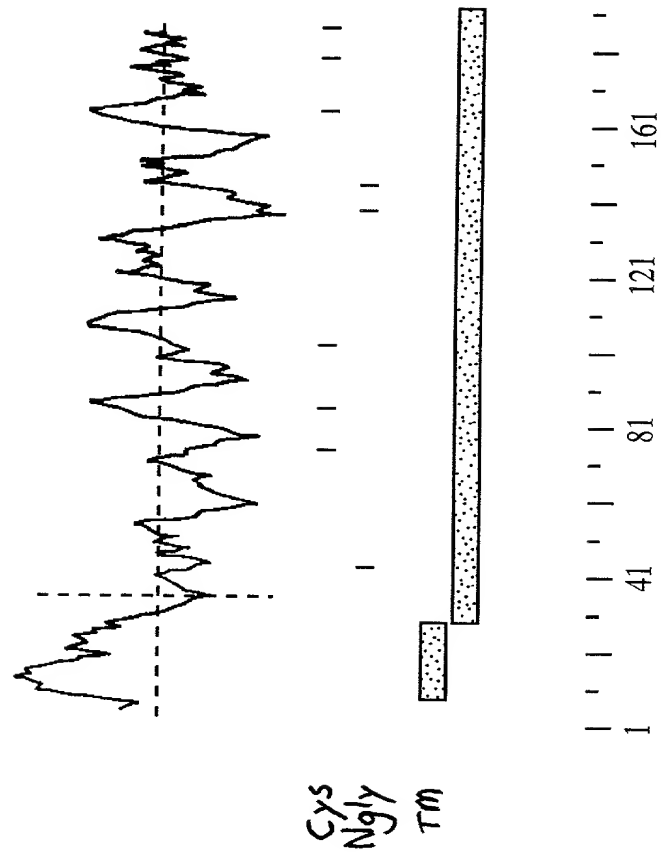


FIG. 11Z-6

L	F	L	G	G	V	G	M	V	G	T	V	A	V	T	V	M	P	Q	19	
G	CTG	TTT	CTT	GGT	GGT	GTT	GGA	ATG	GTG	GGC	ACA	GTG	GCT	ACT	GTC	ATG	CCT	CAG	58	
W	R	V	S	A	F	I	E	N	N	I	V	V	F	E	N	F	W	E	G	39
TGG	AGA	GTG	TCG	GCC	TTC	ATT	GAA	AAC	AAC	AAC	ATC	GTG	GTT	TTT	GAA	AAC	TTC	TGG	GAA	118
L	W	M	N	C	V	R	Q	A	N	I	R	M	Q	C	K	I	Y	D	S	59
CTG	TGG	ATG	AAT	TGC	GTG	AGG	CAG	GCT	AAC	ATC	AGG	ATG	CAG	TGC	AAA	ATC	TAT	GAT	TCC	178
L	L	A	L	S	P	D	L	Q	A	A	R	G	L	M	C	A	A	S	V	79
CTG	CTG	GCT	CTT	TCT	CCG	GAC	CTA	CAG	GCA	GCC	AGA	GGA	CTG	ATG	TGT	GCT	GCT	TCC	GTG	238
M	S	F	L	A	F	M	M	A	I	L	G	M	K	C	T	R	C	T	G	99
ATG	TCC	TTC	TTG	GCT	TTC	ATG	ATG	GCC	ATC	CTT	GGC	ATG	AAA	TGC	ACC	AGG	TGC	ACG	GGG	298
D	N	E	K	V	K	A	H	I	L	L	T	A	G	I	I	F	I	I	T	119
GAC	AAT	GAG	AAG	GTG	AAG	GCT	CAC	ATT	CTG	CTG	ACG	GCT	GGA	ATC	ATC	TTC	ATC	ATC	ACG	358
G	M	V	V	L	I	P	V	S	W	V	A	N	A	I	I	R	D	F	Y	139
GGC	ATG	GTG	GTG	CTC	ATC	CCT	GTG	AGC	TGG	GTT	GCC	AAT	GCC	ATC	ATC	AGA	GAT	TTC	TAT	418
N	S	I	V	N	V	A	Q	K	R	E	L	G	E	A	L	Y	L	G	W	159
AAC	TCA	ATA	GTG	AAT	GTT	GCC	CAA	AAA	CGT	GAG	CTT	GGA	GAA	GCT	CTC	TAC	TTA	GGA	TGG	478

Fig. 12A

T	T	A	L	V	L	I	V	G	G	A	L	F	C	C	V	F	C	C	N	179
ACC	ACG	GCA	CTG	GTG	CTG	ATT	GTT	GGA	GGA	GCT	CTG	TTC	TGC	TGC	GTT	TTT	TGT	TGC	AAC	538
E	K	S	S	S	Y	R	Y	S	I	P	S	H	R	T	T	Q	K	S	Y	199
GAA	AAG	AGC	AGT	AGC	TAC	AGA	TAC	TCG	ATA	CCT	TCC	CAT	CGC	ACA	ACC	CAA	AAA	AGT	TAT	598
H	T	G	K	K	S	P	S	V	Y	S	R	S	Q	Y	V	*				215
CAC	ACC	GGA	AAG	AAG	TCA	CCG	AGC	GTC	TAC	TCC	AGA	AGT	CAG	TAT	GTG	TAG				649
TTGTG	TATG	TTTTT	TAACTTT	TACTATA	AAAGCC	ATGCA	AAAAAT	CTATAT	TACTTT	CTCA	AAAAAT	GGACCC	CAA							728
AGAA	ACTTT	TGATTT	TACTG	TTCTT	AAC	TGCCT	AACTT	TAAT	TACAG	AACTG	TGCAT	CAGCT	ATTT	TATG	ATTCT	ATAAGC				807
TATTT	CAGCAG	AAATG	AGATAT	TAAAC	CCAATG	CTTTG	ATTGTT	CTAG	AAAGT	ATAGT	AAATTTG	TTTCT	TAAG	TGTT	C	TAAGT	GGTTC			886
AAGCA	TCTACT	CTTTT	TATCAT	TTTACT	TCAAA	ATGAC	ATTGCT	AAAG	ACTGC	ATTATTT	TACT	ACTGT	AAATTT	CTCC	CAC					965
GACAT	AGCAT	TATGT	ACATAG	ATGAG	TGTA	ACATTT	ATATCT	CACAT	AGAG	ACATGCT	TATATG	TTTAT	TGTT	TATTT	AAAATG					1044
AAATG	CCAGT	CCATT	ACACT	GAA	TAAAT	AGAACT	CACTATT	GCTTTT	CAGG	AAATCAT	GGATAG	GGTTGA	AGAA	AGGT						1123
TACTAT	TAAAT	TGTTT	AAAAAC	AGCTT	AGGAT	TAAATG	TCTCC	ATTATA	TAAATGA	AGATTAA	AAATGA	AGGCTT	TAAT	CAG						1202
CATTG	TAAAGG	AAATG	AATGG	CTTCT	GATATG	CTGTTT	TTTAG	CCTAGG	AGTTAG	AAATCCT	AACTTCT	TTTAT	CCCTC							1281
TTCTCC	AGAGG	CTTTT	TTTTT	CTTGT	GTATT	TAAATTA	ACATTTT	TAAA	AAAGC	AGATATTT	TGTCA	AGGG	CTTTG	GCAT						1360
TCAA	ACTGCT	TTTCC	AGGCT	ATAC	TCA	GAA	GAAG	ATA	AAAGT	GTGAT	CTA	AGAAAA	AGTG	ATGG	TTTAG	GAAAGT				1439
AAAA	TATTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	1518
AGTAT	TGAGT	ACAG	ACTTT	GAGG	TTT	CATCA	TATA	TAAAT	AAAG	AGCAG	AAAAAT	ATGCT	TGTTT	CATTT	GCCTTA					1597

Fig. 12B

CCAAAAACAACAACAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCA 1676
 TTTTGTCTCTGTGAAAAATAAAATTTCCCTTCTGTACCAATTTCTGTTAGTTTACTAAAAATCTGTAATACTGTATTTT 1755
 TCTGTTTATTCCAAATTTGATGAAACTGACAAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGT 1834
 GTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTCTAAAAAATAAAAAAATAAAAAA 1909

Fig. 12C

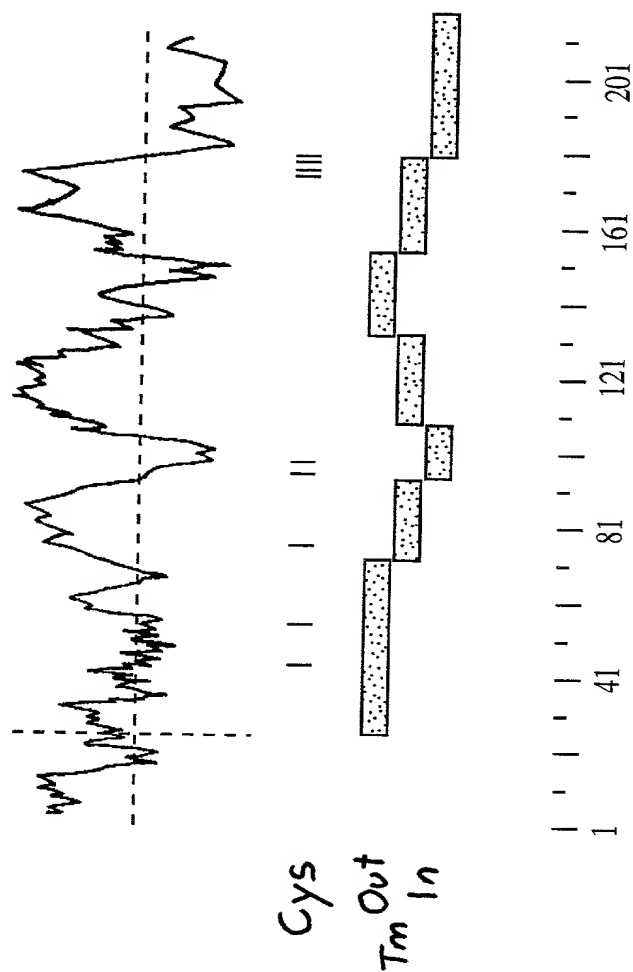


FIG. 12D

```

DKFZ G-----GGGCA-----
:
I309 GCTGTTCTTGGTGGTGGTGGGACACAGTGGCTGTCACTGTCACTGCCTCAGTGGAGAGTGTCG
      10      20      30      40      50      60      70

DKFZ -----

I309 GCCTTCATTGAAAAACAACATCGTGGTTTTTGAAAAACTTCTGGGAAGGACTGTGGATGAATTGCCGTGAGGC
      80      90      100     110     120     130     140

DKFZ -----

I309 AGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGC
      150     160     170     180     190     200     210

DKFZ -----

I309 CAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCCTTCTTGGCTTTCAATGATGGCCATCCTTGGCATGAAA
      220     230     240     250     260     270     280

DKFZ -----

I309 TGCACCAAGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCA
      290     300     310     320     330     340     350

```

Fig. 12E

```

DKFZ -----
I309 TCATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCATATAA
      360      370      380      390      400      410      420
DKFZ -----
I309 CTCAATAGTGAATGTTGCCCAAAAACGTGAGCTTGGAGAAAGCTCTCTACTTAGGATGGACCACGGCACTG
      430      440      450      460      470      480      490
DKFZ -----
I309 GTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAAGCAGTAGCTACAGAT
      500      510      520      530      540      550      560
DKFZ -----
I309 ACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAGTCACCGAGCGTCTACTC
      570      580      590      600      610      620      630
DKFZ -----
I309 CAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAATGACAAAAATC
      640      650      660      670      680      690      700

```

Fig. 12F

```

DKFZ -----
I309 TATATTACTTTCTCAAAATGGACCCCAAGAAACTTTGATTACTGTTCTTAACTGCCTAATCTTAATTA
      710      720      730      740      750      760      770
DKFZ -----
I309 CAGGAACTGTGCATCAGCTATTATGATTCTATAAGCTATTTCAGCAGAAATGAGATATTAAACCCAATGC
      780      790      800      810      820      830      840
      30      40      50      60      70      80      90
DKFZ TTTGATTGTTCTAGAAAAGTATAGTAATTTGTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 TTTGATTGTTCTAGAAAAGTATAGTAATTTGTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTT
      850      860      870      880      890      900      910
      100      110      120      130      140      150      160
DKFZ ACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAAATTTCTCCACGACATAGCATTAATGT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 ACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAAATTTCTCCACGACATAGCATTAATGT
      920      930      940      950      960      970      980

```

Fig. 12G

170	180	190	200	210	220	230
DKFZ	ACATAGATGAGTGTAA	CATTATATCTCACATAGAGACATGCTTATATGGTTTATTTAA	AATGAAATGC			
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
I309	ACATAGATGAGTGTAA	CATTATATCTCACATAGAGACATGCTTATATGGTTTATTTAA	AATGAAATGC			
	990	1000	1010	1020	1030	1040 1050
240	250	260	270	280	290	300
DKFZ	CAGTCCATTACACTGA	ATAAATAGAACTCAACTATTGCTTTTCAGGAAATCATGGATAGGGTTGAAGAA				
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
I309	CAGTCCATTACACTGA	ATAAATAGAACTCAACTATTGCTTTTCAGGAAATCATGGATAGGGTTGAAGAA				
	1060	1070	1080	1090	1100	1110 1120
310	320	330	340	350	360	370
DKFZ	GGTACTATTAAATTTG	TTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGAAGATTAAAAATGA				
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
I309	GGTACTATTAAATTTG	TTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGAAGATTAAAAATGA				
	1130	1140	1150	1160	1170	1180
380	390	400	410	420	430	440
DKFZ	AGGCTTTAATCAGCAT	TGTAAAGGAAATTGAAATGGCTTTCTGATATGCTGTTTTTAGCCTAGGAGTTAG				
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
I309	AGGCTTTAATCAGCAT	TGTAAAGGAAATTGAAATGGCTTTCTGATATGCTGTTTTTAGCCTAGGAGTTAG				
	1190	1200	1210	1220	1230	1240 1250

Fig. 12H

450	460	470	480	490	500	510
DFKZ	AAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTCTTGTGTTAAATTAACATTTTAA					
	::					
I309	AAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTCTTGTGTTAAATTAACATTTTAA					
1260	1270	1280	1290	1300	1310	1320
520	530	540	550	560	570	580
DFKZ	AAAGCAGATATTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTCCAGGGCTATACTCAGAAAGAGATA					
	::					
I309	AAAGCAGATATTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTCCAGGGCTATACTCAGAAAGAGATA					
1330	1340	1350	1360	1370	1380	1390
590	600	610	620	630	640	650
DFKZ	AAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAAATATTTTGTATTTGAAGAAG					
	::					
I309	AAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAAATATTTTGTATTTGAAGAAG					
1400	1410	1420	1430	1440	1450	1460
660	670	680	690	700	710	720
DFKZ	AATGATGCATTTTGACAAGAAATCATATATGTAATGGATATATTTTAATAAGTATTTGAGTACAGACTTG					
	::					
I309	AATGATGCATTTTGACAAGAAATCATATATGTAATGGATATATTTTAATAAGTATTTGAGTACAGACTTG					
1470	1480	1490	1500	1510	1520	1530

Fig. 12I

```

730      740      750      760      770      780      790
DKFZ AGGTTTCATCAATATAAAAGAGCAGAAAATATGCTCTGGTTTTCATTTGCTTACCAAAAAACAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AGGTTTCATCAATATAAAAGAGCAGAAAATATGCTCTGGTTTTCATTTGCTTACCAAAAAACAA
1540 1550 1560 1570 1580 1590 1600

800      810      820      830      840      850      860
DKFZ CAACAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 CAACAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTT
1610 1620 1630 1640 1650 1660 1670

870      880      890      900      910      920      930
DKFZ TTGTTCTGTGAAAAATAAATTCCCTTCTGTACCATTTCTGTTTAGTTTTACTAAATCTGTAATACTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 TTGTTCTGTGAAAAATAAATTCCCTTCTGTACCATTTCTGTTTAGTTTTACTAAATCTGTAATACTG
1680 1690 1700 1710 1720 1730 1740

940      950      960      970      980      990      1000
DKFZ TATTTTCTGTTTATTCCAAATTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGCTGTCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 TATTTTCTGTTTATTCCAAATTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGCTGTCT
1750 1760 1770 1780 1790 1800 1810

```

Fig. 12J

```

1010      1020      1030      1040      1050      1060      1070
DKFZ  AGCTTAAATGAATGTTCTATTGCTTTATACATTATATAATAAATTGTACATTTTCCAAAAAAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309  AGCTTAAATGAATGTTCTATTGCTTTATACATTATATAATAAATTGTACATTTTCTAAAAAAA
1820      1830      1840      1850      1860      1870      1880

1080      1090
DKFZ  AAAAAAAAAA-----
      ::::::::::::::
I309  AAAAAAAAAAAAAAAAAAAAAA
1890      1900

```

Fig. 12K

[illegible]

Fig. 12L

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260      270      280      290      300      310      320
I309 CTTTCATGATGGCCATCCTTGGCATGAAATGCACCAAGTGCACGGGGCAATGAGAAGTGAAAGGCTCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 CTTTCATGACAGCCATCCTCGGAATGAAGTGCACCAAGTGCACGGGGACGATGAGAACGTGAAGAGCCG
      290      300      310      320      330      340      350

330      340      350      360      370      380      390
I309 CATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCAATGGTGGTCTCATCCCTGTGAGCTGGGTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 CATCTTGCTGACAGCCGGAATCATCTTCTTCATCACCGGCTGGTGTGCTCATCCCTGTGAGCTGGGTT
      360      370      380      390      400      410      420

400      410      420      430      440      450      460
I309 GCCAATGCCATCATCAGAGATTTCATAACTCAATAGTGAATGTGCCCAAAAACGTGAGCTTGGAGAAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 GCCAATTCCATCATCAGAGACTTCTACAACCCACTGGTGGATGTGGCCCTAAAGCGCGAGCTGGGAGAAG
      430      440      450      460      470      480      490

470      480      490      500      510      520      530
I309 CTCTCTACTTAGGATGGACCACGGCACTGGTGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTGTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 CCCTCTACATAGGCTGGACCACAGCGCTGGTGTGCTGATCGCTGGAGGAGCACTGTTCTGTTGTGTTTGTG
      500      510      520      530      540      550      560

```

Fig. 12M

540 550 560 570 580 590 600
I309 TTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATACTTCCCATCGCACAAACCCAAAAAGTTATCAC
::: : ::::::::::: : ::::::::::: : ::::::::::: : ::::::::::: : ::::::::::: : ::
CLAUD8 TTGTACTGAAAGGAGCAACAGTTACAGGTACTCGGTACCATCCCATCGCACCACTCAACGGAGTTTCCAC
570 580 590 600 610 620 630
610 620 630 640 650 660 670
I309 ACCGGAAAGAGTCACCGAGCGTCTACTCCAGAAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTT
::::::::::::::::: : ::::::::::: : ::::::::::: : ::::::::::: : ::::::::::: : ::
CLAUD8 GCCGAAAAGAGATCTCCGAGCATATACTCCAAAAGTCAGTATGTGTAG-----
640 650 660 670
680 690 700 710 720 730 740
I309 ACTATAAGCCATGCAAAATGACAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAAACTTTTGATT
CLAUD8 -----
750 760 770 780 790 800 810
I309 TACTGTTCTTAAGTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATT
CLAUD8 -----

Fig. 12N

	820	830	840	850	860	870	880
I 309	TCAGCAGAATGAGATAATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTGTTTTCTAAGGT						
CLAUD8	-----						
	890	900	910	920	930	940	950
I 309	GGTTCAAGCATCTACTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTAC						
CLAUD8	-----						
	960	970	980	990	1000	1010	1020
I 309	TGTAATTTCTCCACGACATAGCATTTATGTACATAGATGAGTGTAACATTTATATCTCACATAGAGACATG						
CLAUD8	-----						
	1030	1040	1050	1060	1070	1080	1090
I 309	CTTATATGGTTTTATTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTT						
CLAUD8	-----						
	1100	1110	1120	1130	1140	1150	1160
I 309	TCAGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAAATGTTAAAAACAGCTTAGGGATTAAATGT						
CLAUD8	-----						

Fig. 120

	1170	1180	1190	1200	1210	1220	1230
I 309	CCTCCATT	TATAATGAAGAT	TAAATGAAGCTT	AATCAGCAT	TGTAAAGGAAA	TTGAATGGCT	TTTCTG
CLAUD8	-----						
	1240	1250	1260	1270	1280	1290	1300
I 309	ATATGCTG	TTTTAGCCTAGGAG	TTAGAAATCCTAACT	TCCTTATCCT	CTCTCCCAGAGG	CTTTT	TTTT
CLAUD8	-----						
	1310	1320	1330	1340	1350	1360	1370
I 309	TTCTTG	TGTAATAACAT	TTTAAAGCAGAT	ATTTGTCAAGGGG	CTTGCATT	CAAACTGCTT	
CLAUD8	-----						
	1380	1390	1400	1410	1420	1430	1440
I 309	TTCCAGGG	CTATACTCAGAA	GAAGATAAAAGT	GTGATCTAAGAAA	AGTGATGTT	TAGGAAAGT	GAA
CLAUD8	-----						

Fig. 12P

```

1450      1460      1470      1480      1490      1500      1510
I309 AATATTTTGTGTTTGTATTGAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATAT
CLAUD8 -----

1520      1530      1540      1550      1560      1570      1580
I309 TTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAATAAAGAGCAGAAAAATATGTCTT
CLAUD8 -----

1590      1600      1610      1620      1630      1640      1650
I309 GGTTTTCATTTGCTTACCACAAAAACACACAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTAT
CLAUD8 -----

1660      1670      1680      1690      1700      1710      1720
I309 GTGGGTACCTGAGTCAAAATTGTCATTTTGTCTGTGAAAAATAAATTTCTTCTTGTACCATTTCTGT
CLAUD8 -----

1730      1740      1750      1760      1770      1780      1790
I309 TTAGTTTACTAAAAATCTGTAAATACTGTATTTTCTGTATTATCCAAATTTGATGAAACTGACAATCCA
CLAUD8 -----

```

Fig. 12Q

	1800	1810	1820	1830	1840	1850	1860
I309	ATTGAAAGTTTGTGTCGACGCTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTATAT						
CLAUD8	-----						
I309	AATAAATTGTACATTTTCTAAAAAATAAAAAAAAAAAAAA						
CLAUD8	-----						

Fig. 12R

CLAUD8	MATYALQMAALVLGGVGMVGTVAVTIMPQWRVS	10	20	30	40	50	60	70
	AFIESNIVVFENRWEGLWMNCMRHANIRMQCKVYDSL							
I309	-----LFLGGVGMVGTVAVTMPQWRVS	10	20	30	40	50	60	
	AFIENNIIVVFENRWEGLWMNCVRQANIRMQCKIYDSL							
CLAUD8	LALSPDLQASRGLMCAASVLAFLAFMTAILGMKCT	80	90	100	110	120	130	140
	CTGDDENVKSRILLTAGIIFITGLVVLIPVSWV							
I309	LALSPDLQAARGLMCAASVMSFLAFMMAILGMKCT	70	80	90	100	110	120	130
	CTGDNKVKAHILLTAGIIFIITGMVVLIPVSWV							
CLAUD8	ANSIIRDFYNPLVDVALKRELGEALYIGWTTALVLI	150	160	170	180	190	200	210
	AGGALFCCVFCCTERSNSYRYSVPSHRTTQRSFH							
I309	ANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLI	140	150	160	170	180	190	200
	VGALFCCVFCCKNEKSSSYRYSIPSHRTTQKSYH							
CLAUD8	AEKRSPSIYSKSQYV	220						
I309	TGKKSPSVYSRSQYV	210						

Fig. 12S

```

I309 .....LFLGGVMVGTVAVTMPQWRVSAFIENNIIVFFENFWEGL 40
hCPE MASMGLQVMGIALAVLGLWLAVMLCCALPMWRVTAFIGSNIIVTSQTIWEGL 50
mCPE MASMGLQVLGISLAVLGLWLGIIILSCALPMWRVTAFIGSNIIVTAQTSWEGL 50
rRPV .MSMSLEITGTS LAVLGLWLC TIVCCALPMWRVSAFIGSSIITAQITWEGL 49

I309 WMNCVRQANIRMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAIL 90
hCPE WMNCVVQSTGQMCKVYDSSLALPQDLQAARALVIISIIVAALGVLLSVV 100
mCPE WMNCVVQSTGQMCKMYDSSLALPQDLQAARALMVISIIVGALGMLLSVV 100
rRPV WMNCV.QSTGQMCKMYDSSLALPQDLQAARALIVSILLAFFGLLVALV 98

I309 GMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIIPVSWVANAIIRDFYN 140
hCPE GGKCTNCLED.ESAKAKTMI VAGVVFLLAGLMVIVPVSWTAHNI IQDFYN 149
mCPE GGKCTNCMED.ETVKAKIMITAGAVFIVASMLIMVPVSWTAHNVIRDFYN 149
rRPV GAQCTNCVQD.ETAKAKITIVAGVLFLLAAVITLVPVSWSANTIIIRDFYN 147

I309 SIVNVAQKRELGEALYLGWTTALVLI VGGALFCCVFCCKNEKSSSYRYSIP 190
hCPE PLVASGQKREMGASLYVGWAAAGLLLLGGGLICC.NCPRTDKPYS AKYS 198
mCPE PMVASGQKREMGASLYVGWAAAGLLLLGGGLCCSCPPRSNDKPYS AKYS 199
rRPV PLVPEAQKREMG TGLYVGWAAAALQLLGGALLCCSCPPREKYAPT KILYS 197

I309 SHRTTQKSYHTGKKSPSVYSRSQYV 215
hCPE AARSAAAASNYV..... 209
mCPE AARSVPASNYV..... 210
rRPV APRSTGPGTGTGTAYDRKTTSERPGARTPHHHHYQPSMYPTRPACSLASET 248

```

Fig. 12T

CGAGCGCGCGCGGCAGGTCAGACATGGGCCAAGAGCCAGAGCCCGTCCGGGGTCTGTGAGTTGAGCTTGAGGCCG 79

M R V I M G I A S L G F L W A V F L 18

CAGG ATG AGG GTC ATC ATG GGG ATA GCC AGC CTG GGG TTC CTC TGG GCA GTA TTC CTG 137

L P L V F G V P T E E T T F G E S V A S 38

CTT CCT CTT GTG TTT GGG GTC CCC ACA GAG GAG ACT ACC TTT GGA GAA TCT GTG GCC TCC 197

H L P K G C R C R C D P E D L M S S D D 58

CAT CTC CCC AAA GGC TGT CGA CGA TGC TGT GAC CCC GAG GAC CTG ATG TCC TCT GAT GAT 257

T V Q A P V S P Y V L P E V R P Y L G R 78

ACG GTC CAG GCC CCT GTT TCC CCT TAT GTC CTG CCT GAA GTC AGG CCG TAC CTC GGC CGC 317

D H 80

GAC CAC 323

Fig. 13A

FIG. 10 DE 163450

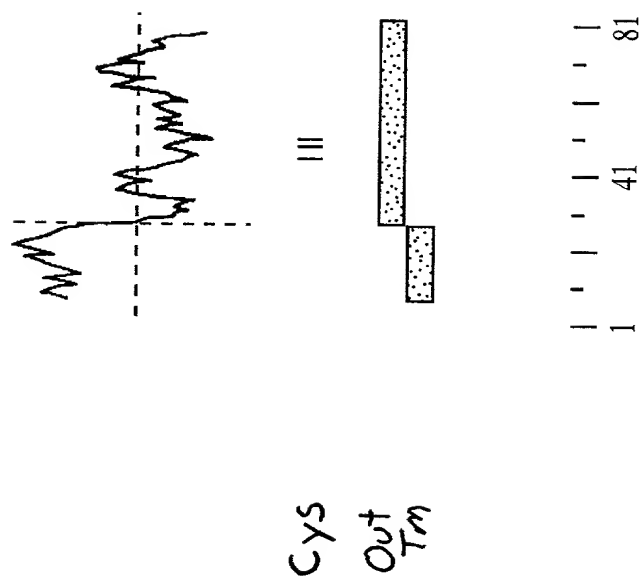


FIG. 13B

CGGACGCGTGGCGGACGCGTGGGGTTATTCTTTGGTTGTAGGTATAATATGGCAATTAAAAACAACACCCAGTTT 79
M E F L Y R I V V G F I L I F T 16
TGTA CTGTGTA AAGT ATG GAA TTC TTA TAT TAT AGG ATT GTT GGT GGA TTC ATT CTT ATC TTT ACA 142
F F N I K G Q N T K C P M S C Y Y I V R 36
TTT TTT AAT ATT AAG GGA CAG AAT ACC AAG TGT CCA ATG TCT TGT TAT TAT ATT GTT AGG 202
V L G T L G I L T V F W V C P L T I F N 56
GTA CTG GGC ACT TTG GGG ATA TTG ACT GTA TTC TGG GTT TGC CCC CTC ACT ATT TTT AAT 262
P D Y F I P I S I T I V L T L L G I L 76
CCA GAC TAT TTT ATA CCT ATC AGT ATA ACT ATA GTT CTT ACT CTT CTT GGA ATT CTT 322
F L I V Y Y G S F H P N R S A E T K C D 96
TTT CTT ATT GTT TAT TAT GGG AGT TTT CAC CCA AAC AGA AGT GCA GAA ACA AAA TGT GAT 382
E I D G K P V L R E C R M R Y F L M E * 115
GAA ATT GAT GGA AAA CCA GTT CTA AGA GAA TGT AGA ATG AGA TAT TTC CTA ATG GAA TAA 442
GCTATTCA TTATGATATATATTTTCTTATATTTTGTTCATTTGGTTAGTAAAGAAAATGTGTGTTAAAAA AAAAAA 521
AAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 546

Fig. 14A

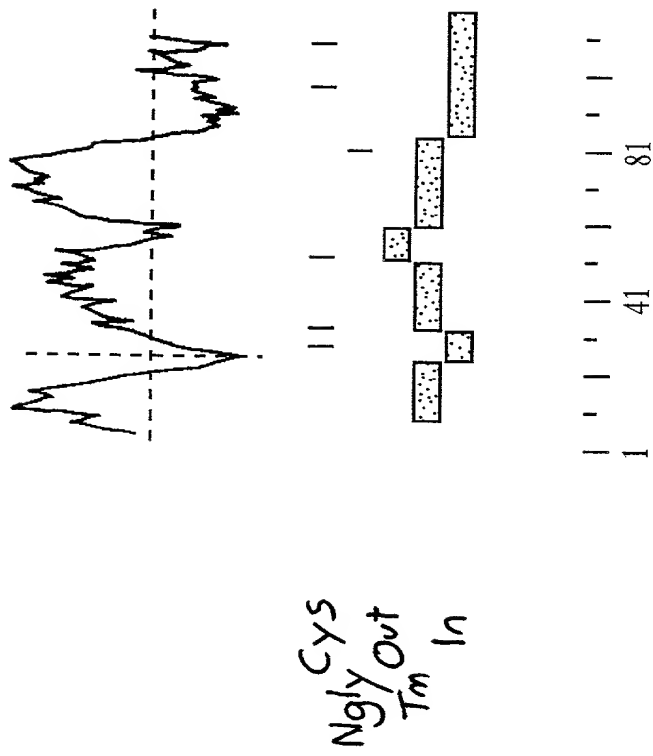


FIG. 14B

CGGACGCGGTGGCGGACGCGTGGGCAGCTGAAGAAAGAGAGGA										ATG AAG CGC CTT CTG CTT CTG TTT										8
																				68
L	F	F	I	T	F	S	S	A	F	P	L	V	R	M	T	E	N	E	E	28
TTG	TTC	TTT	ATA	ACA	TTT	TCT	TCT	GCA	TTT	CCC	TTA	GTC	CGG	ATG	ACG	GAA	AAT	GAA	GAA	128
N	M	Q	L	A	Q	A	Y	L	N	Q	F	Y	S	L	E	I	E	G	N	48
AAT	ATG	CAA	CTG	GCT	CAG	GCA	TAT	CTC	AAC	CAG	TTC	TAC	TCT	CTT	GAA	ATA	GAA	GGG	AAT	188
H	L	V	Q	S	K	N	R	S	L	I	D	D	K	I	R	E	M	Q	A	68
CAT	CTT	GTT	CAA	AGC	AAG	AAT	AGG	AGT	CTC	ATA	GAT	GAC	AAA	ATT	CGG	GAA	ATG	CAA	GCA	248
																				128/361
F	F	G	L	T	V	T	G	K	L	D	S	N	T	L	E	I	M	K	T	88
TTT	TTT	GGA	TTG	ACA	GTG	ACT	GGA	AAA	CTG	GAC	TCA	AAC	ACC	CTT	GAG	ATC	ATG	AAG	ACA	308
P	R	C	G	V	P	D	V	G	Q	Y	G	Y	T	L	P	G	W	R	K	108
CCC	AGG	TGT	GGG	GTG	CCT	GAT	GTG	GGC	CAG	TAT	GGC	TAC	ACC	CTC	CCT	GGG	TGG	AGA	AAA	368
Y	N	L	T	Y	R	I	I	N	Y	T	P	D	M	A	R	A	A	V	D	128
TAC	AAC	CTC	ACC	TAC	AGA	ATA	ATA	AAC	TAT	ACT	CCG	GAT	ATG	GCA	CGA	GCT	GCT	GTG	GAT	428
E	A	I	Q	E	G	L	E	V	W	S	K	V	T	P	L	K	F	T	K	148
GAG	GCT	ATC	CAA	GAA	GGT	TTA	GAA	GTG	TGG	AGC	AAA	GTC	ACT	CCA	CTA	AAA	TTC	ACC	AAG	488

Fig. 15A

I S K G I A D I M I A F R T R V H G R C 168
 ATT TCA AAG GGG ATT GCA GAC ATC ATG ATT GCC TTT AGG ACT CGA GTC CAT GGT CGG TGT 548

 P R Y F D G G P L G V L G H A F P P G P G 188
 CCT CGC TAT TTT GAT GGT CCC TTG GGA GTG CTT GGC CAT GCC TTT CCT CCT GGT CCG GGT 608

 L G G D T H F D E D E N W T K D G A G F 208
 CTG GGT GGT GAC ACT CAT TTT GAT GAG GAT GAA AAC TGG ACC AAG GAT GGA GCA GGA TTC 668

 N L F L V A A H E F G H A L G L S H S N 228
 AAC TTG TTT CTT GTG GCT GCT CAT GAA TTT GGT CAT GCA CTG GGG CTC TCT CAC TCC AAT 728

 D Q T A L M F P N Y V S L D P R K Y P L 248
 GAT CAA ACA GCC TTG ATG TTC CCA AAT TAT GTC TCC CTG GAT CCC AGA AAA TAC CCA CTT 788

 S Q D D I N G I Q S I Y G G L P K V P A 268
 TCT CAG GAT GAT ATC AAT GGA ATC CAG TCC ATC TAT GGA GGT CTG CCT AAG GTA CCT GCT 848

 K P K E P T I P H A C D P D L T F D A I 288
 AAG CCA AAG GAA CCC ACT ATA CCC CAT GCC TGT GAC CCT GAC TTG ACT TTT GAC GCT ATC 908

 T T F R R E V M F F K G R H L W R I Y Y 308
 ACA ACT TTC CGC AGA GAA GTA ATG TTC TTT AAA GGC AGG CAC CTA TGG AGG ATC TAT TAT 968

Fig. 15B

D I T D V E F E L I A S F W P S L P A D 328
 GAT ATC ACG GAT GTT GAG TTT GAA TTA ATT GCT TCA TTC TGC CCA TCT CTG CCA GCT GAT 1028

 L Q A A Y E N P R D K I L V F K D E N F 348
 CTG CAA GCT GCA TAC GAG AAC CCC AGA GAT AAG ATT CTG GTT TTT AAA GAT GAA AAC TTC 1088

 W M I R G Y A V L P D Y P K S I H T L G 368
 TGG ATG ATC AGA GGA TAT GCT GTC TTG CCA GAT TAT CCC AAA TCC ATC CAT ACA TTA GGT 1148

 F P G R V K K I D A A V C D K T T R K T 388
 TTT CCA GGA CGT GTG AAG AAA ATA GAT GCA GCC GTC TGT GAT AAG ACC ACA AGA AAA ACC 1208

 Y F F V G I W C W R F D E M T Q T M D K 408
 TAC TTC TTT GTG GGC ATT TGG TGC TGG AGG TTT GAT GAA ATG ACC CAA ACC ATG GAC AAA 1268

 G F P Q R V V K H F P G I S I R V D A A 428
 GGA TTC CCG CAG AGA GTG GTA AAA CAC TTT CCT GGA ATC AGT ATC CGT GTT GAT GCT GCT 1328

 F Q Y K G F F F F F S R G S K Q F E Y N I 448
 TTC CAG TAC AAA GGA TTC TTC TTT TTC AGC CGT GGA TCA AAG CAA TTT GAA TAC AAC ATT 1388

 K T K N I T R I M R T N T W F Q C K E P 468
 AAG ACA AAG AAT ATT ACC CGA ATC ATG AGA ACT AAT ACT TGG TTT CAA TGC AAA GAA CCA 1448

Fig. 15C

Figure 15D

K	N	S	S	F	G	F	D	I	N	K	E	K	A	H	S	G	G	I	K	488																								
AAG	AAC	TCC	TCA	TTT	GGT	TTT	GAT	ATC	AAC	AAG	GAA	AAA	GCA	CAT	TCA	GGA	GGC	ATA	AAG	1508																								
I	L	Y	H	K	S	L	S	L	F	I	F	G	I	V	H	L	L	K	N	508																								
ATA	TTG	TAT	CAT	AAG	AGT	TTA	AGC	TTG	TTT	ATT	TTT	GGT	ATT	GTT	CAT	TTG	CTG	AAA	AAC	1568																								
T	S	I	Y	Q	*															514																								
ACT	TCT	ATT	TAT	CAA	TAA															1586																								
ATT																				CAT	AGACCT	AAAA	TAA	AA	CCT	CA	AC	GGT	CTTT	TAA	TATA	AAAT	CT	GC	TTCA	AA	ATAG	AA	TAA	AA	CCAT	TTCT	TTAAC	1665
AAC																				AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	1684						

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Fig. 15D

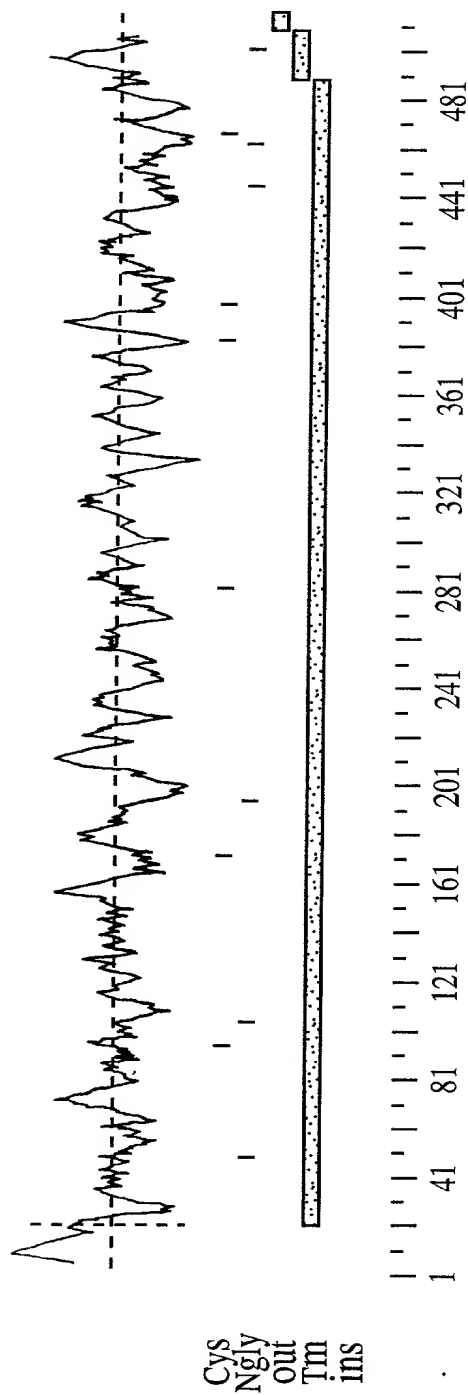


FIG. 15E

GCTTTAACTGAAGACAGGA ATG AAG TGC CTT CTG TCT CTG ATG GTT AAT TTT ATA ACA																13
																60
L S A A F P P D R K D K N E E N N Q L A																33
CTT TCC GCT GCA TTT CCT CCA GAC AGG AAG GAC AAA AAT GAG GAG AAC AAC CAA CTG GCC																120
Q A Y L N Q F Y S L E I E G S H F V Q S																53
CAG GCA TAT CTC AAC CAG TTC TAC TCT CTT GAA ATA GAA GGG AGT CAT TTT GTC CAA AGC																180
K N R S L F D G K L R E M Q A F F G L T																73
AAG AAC AGG AGT CTC TTT GAT GGA AAA CTT CGG GAA ATG CAG GCA TTT TTC GGA TTG ACA																240
V T G K L D S D T L A I M K V P R C G V																133/361
GTG ACT GGA AAA CTG GAT TCA GAC ACA CTT GCG ATC ATG AAA GTG CCC AGG TGT GGG GTA																93/300
P D V G Q Y G Y T L P G W R K Y S L T Y																113
CCA GAT GTG GGG CAA TAT GGC TAC ACA CTC CCT GGG TGG AGA AAA TAC AGC CTT ACA TAC																360
R I M N Y T P D M T P A D V D E A I Q K																133
AGA ATA ATG AAC TAT ACT CCT GAT ATG ACA CCA GCT GAT GTG GAT GAG GCT ATT CAG AAA																420
A L Q V W S K V T P L T F T R I S K G V																153
GCT CTA CAA GTT TGG AGC AAG GTC ACT CCA CTG ACG TTT ACC AGG ATA TCC AAG GGG GTT																480

Fig. 15F

A	D	I	M	I	A	F	R	T	G	V	H	G	W	C	P	R	H	F	D	173
GCA	GAT	ATA	ATG	ATA	GCA	TTC	AGG	ACA	GGA	GTC	CAT	GGC	TGG	TGT	CCT	CGT	CAC	TTT	GAT	540
G	P	L	G	V	L	G	H	A	F	P	P	G	L	G	L	G	G	D	T	193
GGT	CCT	CTG	GGA	GTC	CTT	GGC	CAT	GCC	TTT	CCT	CCT	GGT	CTG	GGT	CTA	GGT	GGT	GAC	ACT	600
H	F	D	E	D	E	T	W	I	A	K	D	G	E	G	F	N	L	F	L	213
CAC	TTT	GAC	GAA	GAT	GAA	ACA	TGG	ATA	GCC	AAG	GAT	GGG	GAA	GGG	TTC	AAC	TTG	TTT	CTT	660
V	A	A	H	E	F	G	H	S	L	G	L	S	H	S	N	D	Q	T	A	233
GTG	GCT	GCT	CAT	GAA	TTT	GGT	CAC	TCT	CTG	GGG	CTG	TCC	CAC	TCC	AAT	GAT	CAA	ACA	GCC	720
L	M	F	P	N	Y	I	S	L	D	P	S	K	Y	P	L	S	Q	D	D	134/253
TTG	ATG	TTC	CCC	AAT	TAC	ATC	TCC	CTG	GAT	CCT	AGC	AAA	TAC	CCA	CTT	TCT	CAG	GAT	GAT	361/780
I	D	G	I	Q	S	I	Y	G	S	P	P	K	V	T	T	K	P	S	G	273
ATT	GAT	GGG	ATC	CAG	TCC	ATC	TAT	GGA	AGT	CCA	CCT	AAG	GTA	ACC	ACC	AAG	CCA	AGT	GGA	840
N	S	E	P	H	A	C	D	P	T	L	T	F	D	A	I	T	T	F	R	293
AAT	TCT	GAA	CCC	CAC	GCC	TGT	GAC	CCC	ACC	TTG	ACT	TTT	GAT	GCT	ATC	ACT	ACT	TTC	CGC	900
R	E	V	M	F	F	K	G	R												302
AGG	GAA	GTT	ATG	TTC	TTT	AAA	GGC	AGG												927

Fig. 15G

TAAACCTATTCCCTTGACACTCCAGCTTCTTATAAAGATGTTTTTTTTTCAAAGGATCTCCGGATAAACAGTCTTCTA	1007
CTCAGCTAGAAAGCCAGTTGCTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCTCAAGAAACAATGTAGAAAAACAA	1087
TCAAAGAAAACACCCCAAGGCAACCTGCAGCTCCACACATAAGCACACATGCATTACATGTATGCCCCACATATGTGA	1167
ACATGTAGGCACACATGCATGCATACCACAAAACCTTAAGACTGAAACATGCTGATGGACACACAGGTACCAGGACA	1247
TCATTGATGAAAATATTTTGTGTTTAATGCAGG	1279
H L W R V Y S D I A G A E F E F I D S F	322
CAC TTA TGG AGG GTC TAC TCT GAT ATT GCT GGT GCT GAG TTT GAG TTT ATT GAT TCC TTC	1339
W P S L P A D L Q A A Y E S P R D E L L	342
TGG CCA TCT CTG CCA GCT GAT CTT CAA GCT GCC TAT GAA AGC CCC AGA GAT GAG CTC CTT	1399
V F K D E N F W V I R G Y S V L P G Y P	362
GTT TTT AAA GAT GAG AAT TTC TGG GTC ATC AGG GGA TAT TCT GTC TTG CCC GGT TAC CCC	1459
K S I H T L G F P R R V K K I D A A V C	382
AAA TCC ATC CAC ACA CTC GGA TTT CCA AGA CGT GTG AAG AAA ATT GAT GCA GCC GTC TGT	1519
D H D T R K T F F F V G I W C W R Y D E	402
GAT CAT GAT ACA AGA AAA ACC TTC TTT TTT GTT GGC ATC TGG TGC TGG AGG TAT GAT GAG	1579
M A Q A M D R G G F P Q R I I K C F P G I	422
ATG GCA CAA GCA ATG GAC AGA GGA TTC CCA CAG AGG ATA AAG TGC TTC CCA GGA ATT	1639

Fig. 15H

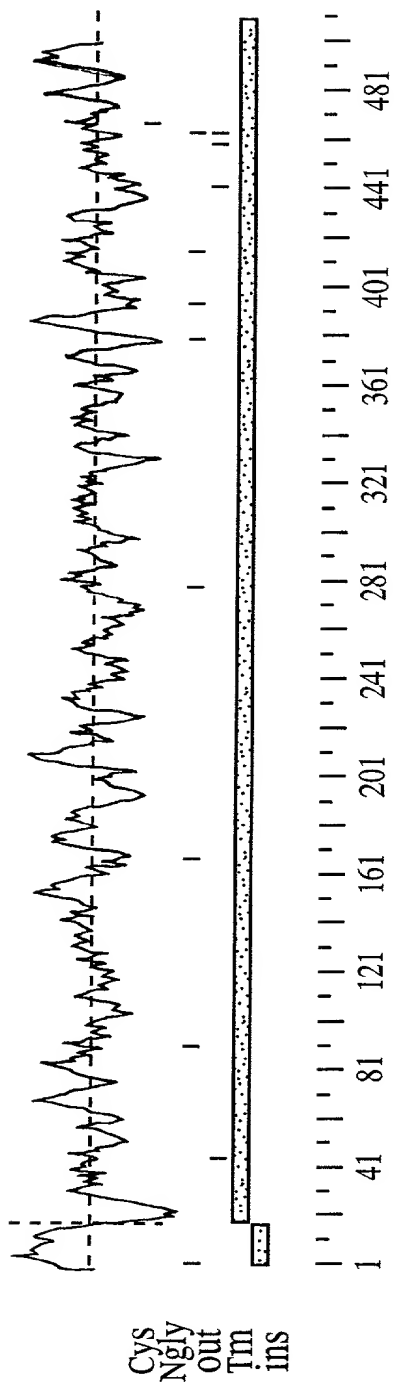


FIG. 15J

Fig. 15K

Fig. 15L

Fig. 15M

human 290 300 310 320 330 340 350
CTCAAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGGCTACACC
murine 260 270 280 290 300 310 320
TTCAGACACACTTGGGATCATGAAAGTGTGGGTACCCAGGTGTGGGTACCCAGATGTGGGGCAATATGGCTACACA

human 360 370 380 390 400 410 420
CTCCCTGGGTGGAGAAATACAACCTCACCTACAGAAATAATAACTATACTCCGGATATGGCACGAGCTG
murine 330 340 350 360 370 380 390
CTCCCTGGGTGGAGAAATACAGCCTTACATACAGAAATAATGAACCTATACTCTGATATGACACGAGCTG

human 430 440 450 460 470 480 490
CTGTGGATGAGGCTATCCAAGAAAGTTTAGAAGTGTGGAGCAAAGTCACTCCACTAAATTCACCAAGAT
murine 400 410 420 430 440 450 460
ATGTGGATGAGGCTATTCAGAAAGCTCTACAAGTTTGGAGCAAAGTCACTCCACTGACGTTTACCAGGAT

human 500 510 520 530 540 550 560
TTCAAAGGGGATTGCAGACATCATGATTTGCCCTTTAGGACTCGAGTCCATGGTGGTGTCTCGCTATTTT
murine 470 480 490 500 510 520 530
ATCCAAGGGGTTGCAGATATAATGATAGCATTCAGGACAGGAGTCCATGGGTGTCTCGTCACTTT

Fig. 15N

Fig. 150

```

840      850      860      870      880      890      900
human  AGGTACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCCTGTGACCCCTGACTTGACTTTTGACGCTAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine AGGTAACCAACCAAGCCAAGTGGAATTCGAAACCCACGCTGTGACCCACCTTGACTTTTGATGCTAT
820      830      840      850      860      870      880

      910      920      930      940
human  CACAACCTTCCGCAGAGAAAGTAATGTTCTTTAAAGGCAGG-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine CACTACTTTCGCGAGGGAAGTTATGTTCTTTAAAGCAGGTAAACCTATTCCCTTGACACTCCAGCTTCT
890      900      910      920      930      940      950

-----
human

murine TATAAAGATGTTTTTTTTTTTCAAAAGGATCTCCGGATAAACAGTCTTCTACTCAGCTAGAAAGCCAGTTG
960      970      980      990      1000      1010      1020

-----
human

murine CTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCCTCAAGAAACAATGTAGAAACAATCAAAGAAAA
1030      1040      1050      1060      1070      1080      1090

```

Fig. 15P

human	1050	1060	1070	1080	1090	1100	1110
	GAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTCTTG						
murine	1380	1390	1400	1410	1420	1430	1440
	AAGCCCAAGAGATGAGCTCCTTGTTTTAAAGATGAGAAATTTCTGGGTGATCAGGGGATATTTCTGTCTTG						
human	1120	1130	1140	1150	1160	1170	1180
	CCAGATTATCCCAAATCCATCCATACATTAGGTTTTCAGGACGTGTGAAGAAAATAGATGCAGCCGCTCT						
murine	1450	1460	1470	1480	1490	1500	1510
	CCCGGTTACCCCAAATCCATCCACACACTCGGATTTCCAAGACGTGTGAAGAAAATTTGATGCAGCCGCTCT						
human	1190	1200	1210	1220	1230	1240	1250
	GTGATAAGACCACAAGAAAAACCTACTTCTTTGTGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCA						
murine	1520	1530	1540	1550	1560	1570	1580
	GTGATCATGATACAAGAAAAACCTTCTTTTGTGGCATCTGGTGCTGGAGGTATGATGAGATGGCACA						
human	1260	1270	1280	1290	1300	1310	1320
	AACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAAACACTTTCCTGGAATCAGTATCCGTTGATGCT						
murine	1590	1600	1610	1620	1630	1640	1650
	AGCAATGGACAGAGGATTCCCAAGAGGATAATAAAGTGCTTCCAGGAATTCGCCCTCCGTTGATGCT						

Fig. 15R

```

950
human  -----
murine CACCCAAGGGCAACCTGCAGCCTCCACACATAAGCACACATGCATTTCACATGTATGCCCCACATATGTGA
1100      1110      1120      1130      1140      1150      1160

human  -----
murine ACATGTAGGCACACATGCATGCATACCAAAACCACAAACTTAAGACTGAAACATGCTGATGGACACAGG
1170      1180      1190      1200      1210      1220      1230

human  -----
          960      970
          -----CACCTATGGAGGATCTATTATGATATCA
murine  TACCAGGACATCATTTGATGAAAATATTTTGTGTTTAATGCAGGCACCTTATGGAGGGTCTACTCTGATATTG
1240      1250      1260      1270      1280      1290      1300
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
human  CGGATGTTGAGTTTGAATTAATTGCTTCATCTCGCCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine CTGGTGCTGAGTTTGAGTTTATGATTCCTTCTGGCCCATCTCTGCCAGCTGATCTTCAAGCTGCCTATGA
1310      1320      1330      1340      1350      1360      1370

```

Fig. 15Q

Fig. 15S

Fig. 15T

```

1670
human  TAACAACAA-----
      ::::::::::
murine TAGCATCAAGTTCTTACTCCTACTATATACAGTGGGTAACCAATAACCAGTTAAAGTATCTGATTCTTT
      2220  2230  2240  2250  2260  2270  2280

human  -----

murine CTAACAGTGAAGTTTAAATATGACAAAAATCTCTCACTTATTTTGAGTCTAATTAATGATTGCAAACT
      2290  2300  2310  2320  2330  2340  2350

human  -----

murine TGGAAAAATTAAAGCATGTCTTAAAAATAAACATTAAAGACAAATTCTTAATCCAAAAAATAAAAAA
      2360  2370  2380  2390  2400  2410  2420

human  -----1680
      -----AAAAAATAAAAAA
      ::::::::::::::
murine AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
      2430  2440  2450  2460

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Fig. 15U

Fig. 15V

[illegible]

Fig. 15W

locus_000000000

```

10      20      30      40      50      60
210 ATGAAGCGCCTTCT---GCTTCTGTTTTTTGTTCTTTTATAACATTTTCT-TCTGCAATTCCCTTAGTCCG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGTT-CTCCCTGAAGACGCTTCCATTTCTGCTCTTACTC-CATGTGCAGATTTCCCAAGGCCCTT--TCCT
      10      20      30      40      50      60

70      80      90      100     110     120     130
210 GATGACGGAATAATGAAGAAAATA-TGCAACTGGCTCAGGCATATCTCAACCAGTTCTACTCTCTTGAAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 G-TATCTTCTAAAGAGAAAAATACAAAAACTGT-TCAGGACTACCTGGAAAAAGTTCTAC-CAATTACCAA
      70      80      90      100     110     120     130

140     150     160     170     180     190     200
210 AGAAG-GGAATCATCTTGTTCAAAAGCAAGAATAG--GAGTCTCATAGATGACAAAAATTCGGGAAATGCA
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
MMP-8 GCAACCAGTATCAG--TCTACAAGG-AAGAAATGGCACTAATGTGATCGTTGAAAAAGCTTAAAGAAATGCA
      140     150     160     170     180     190     200

210     220     230     240     250     260     270
210 AGCATTTTTTGGATTGACAGTACTGGAAAACTGGACTCAAACACCCCTTGAGATCATGAAGACACCCAGG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 GCGATTTTTTGGTTGAATGTACGGGGAAGCCAAATGAGGAAACTCTGGACATGATGAAAAAGCCTCGC
      210     220     230     240     250     260     270

```

Fig. 15X-1

Fig. 15X-2

Fig. 15X-3

Fig. 15X-4

```

1100      1110      1120      1130      1140      1150      1160
210 TAGGTTTCCAGGACGTGTGAAGAAAATAGATGCAGCCGTCGTGATAAGACCACAAGAAAAACCTACTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGGCTTCCCAGCAGCGTCCAAGCAATTGACGCAGC-----TGTTTTCTACAGAAGTAAACATACTT
      1110      1120      1130      1140      1150      1160

1170      1180      1190      1200      1210      1220      1230
210 CTTTGTGGGCATTGTGTCTGGAGGTTTGATGAAATGACCCAAACCATGACAAAGGATTCCCGCAGAGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CTTTGTAAATGACCAATTTCTGGAGATATGAT-----AACCAAAGACAATT-----CATGGAGC
      1170      1180      1190      1200      1210

1240      1250      1260      1270      1280      1290      1300
210 GTGGTAAACACTTTCCTGGAATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTCTTCTTTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CAGGT-----TATCCCAAAGCA-TATC-----AGGTGC--CTTTCAGGAATAGAGAGTAA-----
      1220      1230      1240      1250      1260

1310      1320      1330      1340      1350      1360      1370
210 TCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAAGACAAAGAATATTACCCGAATCATGAGAACTAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 -----GTTGAT----GCAGTTT---TCCAGCA-----AGAACATTTC---TTC-----
      1270      1280      1290      1300

```

Fig. 15X-5

```

1380      1390      1400      1410      1420      1430      1440
210 TACTTGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTGATATCAACAAGGAAAAGCACAT
MMP-8  --CATG----TC--TTCAGTGGACCAAGATATTACGCATTTGATCTT-ATTGCT-CAGAGAGTTA-C-----
1310      1320      1330      1340      1350
1450      1460      1470      1480      1490      1500      1510
210 TCAGGAGGCATAAAGATATTGTATCATAGAGTTTAAGCTTGTTTATTTTGGTATTGTTCAATTGCTGA
MMP-8  -CAGA-----GTTGCAAGAG-----GCA-----ATAAATGG-----C-TTAACTGT
1360      1370      1380      1390
1520      1530
210 AAAACACTTCTATTATCAA
MMP-8  AGA-----TATGGC--
1400

```

Fig. 15X-6

GAAAGCGCTGCGGAGGGCCCGGGCCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCC 79
 M P W P L L L L L L A V S G A Q T T R 18
 CCCACC ATG CCG TGG CCC CTG CTG CTG CTG GGC GTG AGT GGC GCC CAG ACA ACC CGG 139
 P C F P G C Q C E V E T F G L F D S F S 38
 CCA TGC TTC CCC GGG TGC CAA TGC GAG GTG GAG ACC TTC GGC CTT TTC GAC AGC TTC AGC 199
 L T R V D C S G L G P H I M P V P I P L 58
 CTG ACT CGG GTG GAT TGT AGC GGC CTG GGC CCC CAC ATC ATG CCG GTG CCC ATC CCT CTG 259
 D T A H L D L S S N R L E M V N E S V L 78
 GAC ACA GCC CAC TTG GAC CTG TCC AAC CGG CTG GAG ATG GTG AAT GAG TCG GTG TTG 319
 A G P G Y T T L A G L D L S H N L L T S 98
 GCG GGG CCG GGC TAC ACG ACG TTG GCT GGC CTG GAT CTC AGC CAC AAC CTG CTC ACC AGC 379
 I S P T A F S R L R Y L E S L D L S H N 118
 ATC TCA CCC ACT GCC TTC TCC CGC CTT CGC TAC CTG GAG TCG CTT GAC CTC AGC CAC AAT 439
 G L T A L P A E S F T S S P L S D V N L 138
 GGC CTG ACA GCC CTG CCA GCC GAG AGC TTC ACC AGC TCA CCC CTG AGC GAC GTG AAC CTT 499

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Fig. 16A

S	H	N	Q	L	R	E	V	S	V	S	A	F	T	T	H	S	Q	G	R	158
AGC	CAC	AAC	CAG	CTC	CGG	GAG	GTC	TCA	GTG	TCT	GCC	TTC	ACG	ACG	CAC	AGT	CAG	GGC	CGG	559
A	L	H	V	D	L	S	H	N	L	I	H	R	L	V	P	H	P	T	R	178
GCA	CTA	CAC	GTG	GAC	CTC	TCC	CAC	AAC	CTC	ATT	CAC	CGC	CTC	GTG	CCC	CAC	CCC	ACG	AGG	619
A	G	L	P	A	P	T	I	Q	S	L	N	L	A	W	N	R	L	H	A	198
GCC	GGC	CTG	CCT	GCG	CCC	ACC	ATT	CAG	AGC	CTG	AAC	CTG	GCC	TGG	AAC	CGG	CTC	CAT	GCC	679
V	P	N	L	R	D	L	P	L	R	Y	L	S	L	D	G	N	P	L	A	218
GTG	CCC	AAC	CTC	CGA	GAC	TTG	CCC	CTG	CGC	TAC	CTG	AGC	CTG	GAT	GGG	AAC	CCT	CTA	GCT	739
V	I	G	P	G	A	F	A	G	L	G	G	L	T	H	L	S	L	A	S	238
GTC	ATT	GGT	CCG	GGT	GCC	TTC	GCG	GGG	CTG	GGA	GGC	CTT	ACA	CAC	CTG	TCT	CTG	GCC	AGC	799
L	Q	R	L	P	E	L	A	P	S	G	F	R	E	L	P	G	L	Q	V	258
CTG	CAG	AGG	CTC	CCT	GAG	CTG	GCG	CCC	AGT	GGC	TTC	CGT	GAG	CTA	CCG	GGC	CTG	CAG	GTC	859
L	D	L	S	G	N	P	K	L	N	W	A	G	A	E	V	F	S	G	L	278
CTG	GAC	CTG	TCG	GGC	AAC	CCC	AAG	CTT	AAC	TGG	GCA	GGA	GCT	GAG	GTG	TTT	TCA	GGC	CTG	919
S	S	L	Q	E	L	D	L	S	G	T	N	L	V	P	L	P	E	A	L	298
AGC	TCC	CTG	CAG	GAG	CTG	GAC	CTT	TCG	GGC	ACC	AAC	CTG	GTG	CCC	CTG	CCT	GAG	GCG	CTG	979

Fig. 16B

L L H L P A L Q S V S V G Q D V R C R R 318
 CTC CTC CAC CTC CCG GCA CTG CAG AGC GTC AGC GTG GGC CAG GAT GTG CGG TGC CGG CGC 1039

 L V R E G T Y P R R P G S S P K V A L H 338
 CTG GTG CGG GAG GGC ACC TAC CCC CGG AGG CCT GGC TCC AGC CCC AAG GTG GCC CTG CAC 1099

 C V D T R E S A A R G P T I L * 354
 TGC GTA GAC ACC CGG GAA TCT GCT GCC AGG GGC CCC ACC ATC TTG TGA 1147

 CAAATGGTGTGCCCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCCTCAGGTCCCGAGTAACTTATGTTCAATGTG 1226
 CCAACACAGGGGGAGCCCGCAGGCCTATGTGGCAGCGTCACCAACAGAGATTGTGGCCCTAGGAGAGGCTTTTGACCT 1305
 GGGAGCCACACCTAGGAGCAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGC 1384
 CAAACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCAAGTGCCCTTCCCTCATGCCCTGGGCCCGGCTG 1463
 ACCCGCAATGGCAGAGGGTGGGTGGGACCCCCCTGCTGCAGGGCAGAGTTCAGGTCACCTGGCTGAGTGTCCCCCTGG 1542
 GCCCATGGCCAGTCACTCAGGGGCGAGTTTCTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTT 1621
 CATCCTTTTCTATTCCCTAGAAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCCTTCTCATGTGACAGAT 1700
 GGGGAAACTGAGGCCCTTGAGAAAGGAAAGGCTAATCTAAGTTCCTGCGGCGAGTGCGATGACTGGAGCACAGCCCTCCT 1779
 GCCTCCCAGCCCGACCAATGCACCTTCTCTGTCTCTCTAATAAGCCCCACCTCCCGCCCTGGGCTCCCCCTTGCTGC 1858
 CCTTGCCCTGTTCCCCATTAGCACAGGAGTAGCAGCAGCAGGACAGGCAAGAGCCCTCAAGTGGGACTCTGGGCCCTCTG 1937
 ACCAGCTGTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTTCCAGCCCTAGC 2016
 CAGTTTCTCACCCCTGGGTTCGCCAGCATCCAGACTGGAACCTACCCATTTCCTCCCTGAGCATCCTCTAGATG 2095
 CTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCATCTGGCTGGGATCTCCAAGGGCCCTCCTGGATTCAAGTCCCCACT 2174
 GGCCCTGAGCACGACAGCCCTTCTTACCCCTCCAGGAATGCCGTGAAGGAGACAAGGTCTGCCCGACCCCATGTCTATG 2253

Fig. 16C

CTCTACCCAGGGCAGCATCTCAGCTTCCGAACCCCTGGGCTGTTCCCTTAGTCTTCAATTTATAAAAGTTGTGCTT 2332
 TTTAACGGAGTGTCACCTTCAACCGGCTCCCCCTACCCCTGCTGCCGGGATGGAGACATGTCATTTGTAAAGCAGA 2411
 AAAAGGTGCAATTTGTTCACTTTTGTAAATATTGTCCCTGGCCCTGTGTTGGGGTGTGGGGAAGCTGGGCATCAGTGGC 2490
 CACATGGGCATCAGGGGCTGGCCCAAGAGACCCCAAGGAGTGTGCTCTTCCCCACCTGCTAGCCCATC 2569
 ATCTATCTAACCGGTCCCTTGATTTAATAAACACTATAAAAGTTAAAAA

Fig. 16D

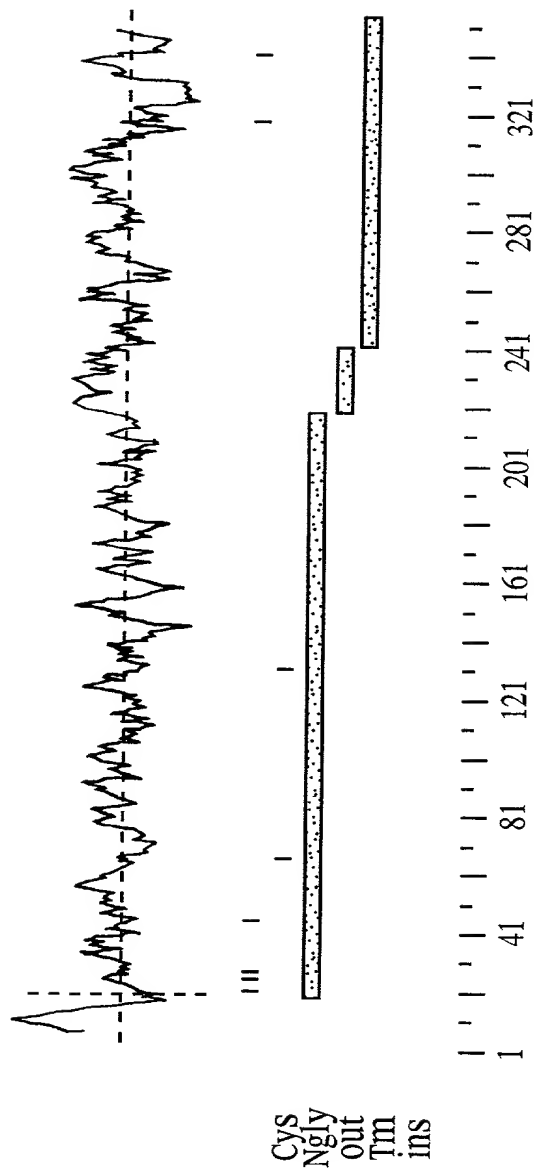


FIG. 16E

GTCGACCCACGCTCCGCCCGGCTAGCGCCGGGTGCGCGAGCCGAGCCGAGCGGCGGAGCCTC	79
TGGAATCACCCGGGTCGCTGTTCTGAGGTGGTCAAGGTGGACAGGGCGGTGATGCGCAGTTTGACACTGAAT	158
ACCAGCGCTAGAGGCCTCCTATAGTATTACACCCCGAGGGAGGACCTGTTGGTGCACGTCGCCGAGGGAGCAA	237
GTCACCTTGGCACCATATTGAACCTTGACCTCTTCTCTCGAGTTTATAATCTGCACCAAGAATGGCTTCACA	316
M L I G E I F E L M Q F L F V V A F T	19
TGT ATG CTC ATC GGG GAG ATC TTT GAG CTC ATG CAG TTC CTC TTT GTG GTT GCC TTC ACT	376
T F L V S C V D Y D I L F A N K M V N H	39
ACC TTC CTG GTC AGC TGC GTG GAC TAT GAC ATC CTA TTT GCC AAC AAG ATG GTG AAC CAC	436
S L H P T E P V K V T L P D A F L P A Q	59
AGT CTT CAC CCT ACT GAA CCC GTC AAG GTC ACT CTG CCA GAC GCC TTT TTG CCT GCT CAA	496
V C S A R I Q E N G S L I T I L V I A G	79
GTC TGT AGT GCC AGG ATT CAG GAA AAT GGC TCC CTT ATC ACC ATC CTG GTC ATT GCT GGT	556
V F W I H R L I K F I Y N I C C Y W E I	99
GTC TTC TGG ATC CAC CGG CTT ATC AAG TTC ATC TAT AAC ATT TGC TGC TAC TGG GAG ATC	616
H S F Y L H A L R I P M S A L P Y C T W	119
CAC TCC TTC TAC CTG CAC GCT CTG CGC ATC CCT ATG TCT GCC CTT CCG TAT TGC ACG TGG	676

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Fig. 17A

Q	E	V	Q	A	R	I	V	Q	T	Q	K	E	H	Q	I	C	I	H	K	139
CAA	GAA	GTG	CAG	GCC	CGG	ATC	GTG	CAG	ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	736
R	E	L	T	E	L	D	I	Y	H	R	I	L	R	F	Q	N	Y	M	V	159
CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	CAC	CGC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	796
A	L	V	N	K	S	L	L	P	L	R	F	R	L	P	G	L	G	E	A	179
GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	856
V	F	F	T	R	G	L	K	Y	N	F	E	L	I	L	F	W	G	P	G	199
GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	916
S	L	F	L	N	E	W	S	L	K	A	E	Y	K	R	G	G	Q	R	L	219
TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	976
E	L	A	Q	R	L	S	N	R	I	L	W	I	G	I	A	N	F	L	L	239
GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	1036
C	P	L	I	L	I	W	Q	I	L	Y	A	F	F	S	Y	A	E	V	L	259
TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	1096
K	R	E	P	G	A	L	G	A	R	C	W	S	L	Y	G	R	C	Y	L	279
AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	1156

Fig. 17B

R H F N E L E H E L E L Q S R L N R G Y K P 299
 CGC CAC TTC AAC GAG CTG GAG CAC GAG CTG CAG TCC CGC CTC AAC CGT GGC TAC AAG CCC 1216

 A S K Y M N C F L S P L L T L A K N G 319
 GCC TCC AAG TAC ATG AAT TGC TTC TTG TCA CCT CTT TTG ACA CTG CTG GCC AAG AAT GGA 1276

 A F F A G S I L A V L I A L T I Y D E D 339
 GCC TTC TTC GCT GGC TCC ATC CTG GCT GTG CTT ATT GCC CTC ACC ATT TAT GAC GAA GAT 1336

 V L A V E H V L T T V T L L G V T V T V 359
 GTG TTG GCT GTG GAA CAT GTG CTG ACC ACC GTG ACA CTC CTG GGC GTC ACC GTG ACC GTG 1396

 C R S F I P D Q H M V F C P E Q L L R V 379
 TGC AGG TCC TTT ATC CCG GAC CAG CAC ATG GTG TTC TGC CCT GAG CAG CTG CTC CGC GTG 1456

 I L A H I H Y M P D H W Q G N A H R S Q 399
 ATC CTC GCT CAC ATC CAC TAC ATG CCT GAC CAC TGG CAG GGT AAT GCC CAC CGC TCG CAG 1516

 T R D E F A Q L F Q Y K A V F I L E E L 419
 ACC CGG GAC GAG TTT GCC CAG CTC TTC CAG TAC AAG GCA GTG TTC ATT TTG GAA GAG TTG 1576

 L S P I V T P L I L I F C L R P R A L E 439
 CTG AGC CCC ATT GTC ACA CCC CTC ATC CTC ATC TTC TGC CTG CGC CCA CGG GCC CTG GAG 1636

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Fig. 17C

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I	I	D	F	F	R	N	F	T	V	E	V	G	V	G	D	T	C	S	459	
ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	1696
F	A	Q	M	D	V	R	Q	H	G	H	P	Q	W	L	S	A	G	Q	T	479
TTT	GCT	CAG	ATG	GAT	GTT	CGC	CAG	CAT	GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	1756
E	A	S	V	Y	Q	Q	A	E	D	G	K	T	E	L	S	L	M	H	F	499
GAG	GCC	TCA	GTG	TAC	CAG	CAA	GCT	GAG	GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	1816
A	I	T	N	P	G	W	Q	P	P	R	E	S	T	A	F	L	G	F	L	519
GCC	ATC	ACC	AAC	CCT	GGC	TGG	CAG	CCA	CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC	1876
K	E	Q	V	Q	R	D	G	A	A	A	S	L	A	Q	G	G	L	L	P	539
AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	GCT	GCT	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	1936
E	N	A	L	F	T	S	I	Q	S	L	Q	S	E	S	E	P	L	S	L	559
GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	1996
I	A	N	V	V	A	G	S	S	C	R	G	P	P	L	P	R	D	L	Q	579
ATC	GCA	AAT	GTG	GTA	GCT	GGC	TCA	TCC	TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	2056
G	S	R	H	R	A	E	V	A	S	A	L	R	S	F	S	P	L	Q	P	599
GGC	TCC	AGG	CAC	AGG	GCT	GAA	GTC	GCC	TCT	GCC	CTG	CGC	TCC	TTC	TCC	CCG	CTG	CAA	CCC	2116

Fig. 17D

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E	P	V	P	E	E	G	S	E	D	E	L	P	P	Q	V	H	K	V	*	
GAG	CCC	GTG	CCC	GAA	GAG	GGC	TCG	GAG	GAT	GAG	CTA	CCC	CCT	CAG	GTG	CAC	AAG	GTA	TAG	2656
ACA	AGG	CTG	AGC	AGG	TT	CC	TG	TG	CCC	CAG	GAT	GG	AG	CC	CG	CT	GC	CA	TG	2735
CTC	CT	CT	AG	TG	TT	CC	CT	GG	CCC	AC	GT	GT	GT	TT	TG	TG	CT	GC	CA	2814
TTG	CC	AC	AG	CCC	CAG	AG	AG	GA	TT	TG	GG	CC	TAG	GA	AC	CG	GA	CT	CA	2893
TTG	GC	TC	AG	AG	TG	GT	CT	AG	AA	CT	GT	CC	CC	AG	CC	CA	GT	TA	CC	2972
CCC	AG	GG	CT	GC	CA	CG	AT	AG	AG	CT	GC	CA	CT	GT	GC	CA	CT	TA	CC	3051
CCCT	CA	AC	CC	CT	GC	AA	CC	TT	CA	AT	AG	AT	AG	CA	GT	GC	CA	CT	TA	3130
TCG	CC	CA	GT	GC	TG	CA	CC	GG	CT	CA	CT	CT	CC	GT	TT	GC	CA	CT	TA	3209
GT	TC	GT	TC	CC	GT	TC	GG	CT	TT	TG	CT	TT	GC	GT	TT	AG	GT	GC	CA	3288
AT	TT	TG	AC	TA	AA	AG	AG	TT	CT	AA	AT	TG	AG	AG	CA	GT	GC	CA	CT	3367
TGG	CC	CC	CC	AG	AG	AC	TG	AG	GT	CT	TC	CT	GG	CC	CT	CA	TT	TG	CT	3446
CCG	GC	TG	AG	GG	TG	AC	CT	CC	AG	CA	AA	AG	AG	CT	TC	GG	CA	CT	GC	3525
AT	GA	AG	GC	GA	TG	CC	CG	AG	GG	CT	TT	TG	GC	CT	GT	GC	CA	CT	GC	3604
CAC	CA	GT	GT	CC	GG	CT	TT	TG	GC	AG	AT	TG	CG	CT	GC	CA	CT	GC	CA	3683
AC	AG	CT	TG	ATA	AC	CT	TA	ATA	AAA	AG	GG	AG	TT	TG	AC	CA	GA	AAAA	AAAA	3762
GCG	GCC	CGC																		3770

Fig. 17F

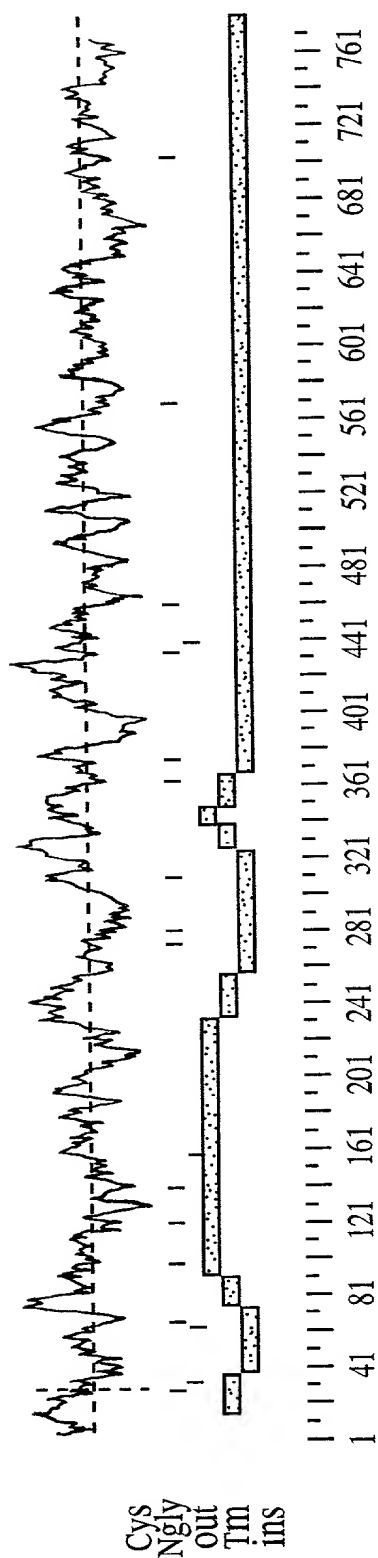


FIG. 176

[illegible]

CCCGGCTAGCGCCGGGTCCGCGCCGAGCCGAGCCGAGCGGAGCCTCTGGAATCACCCGGGTGG 79

	M	A	Q	F	D	T	E	Y	Q
CTGTTCTGAGGTGGTCAAGGTGGACAGGGGGCGGTGGTG	ATG	GCG	CAG	TTT	GAC	ACT	GAA	TAC	CAG

R L E A S Y S D S P G E E D L L V H V 29
 CGC CTA GAG GCC TCC TAT AGT GAT TCA CCC CCA GGG GAG GAG GAC CTG TTG GTG CAC GTC 206

A	E	G	S	K	S	P	W	H	H	I	E	N	L	D	L	F	F	S	R	49
GCC	GAG	GGG	AGC	AAG	TCA	CCT	TGG	CAC	CAT	ATT	GAA	AAC	CTT	GAC	CTC	TTC	TTC	TCT	CGA	266

[illegible]

L	M	Q	F	L	F	V	V	A	F	T	T	F	L	V	S	C	V	D	Y	89
CTC	ATG	CAG	TTC	CTC	TTT	GTG	GTT	GCC	TTC	ACT	ACC	TTC	CTG	GTC	AGC	TGC	GTG	GAC	TAT	386

[illegible][illegible]

Fig. 17H

G	S	L	I	T	I	L	V	I	A	G	V	F	W	I	H	R	L	I	K	149
GGC	TCC	CTT	ATC	ACC	ATC	CTG	GTC	ATT	GCT	GGT	GTC	TTC	TGG	ATC	CAC	CGG	CTT	ATC	AAG	566
F	I	Y	N	I	C	C	Y	W	E	I	H	S	F	Y	L	H	A	L	R	169
TTC	ATC	TAT	AAC	ATT	TGC	TGC	TAC	TGG	GAG	ATC	CAC	TCC	TTC	TAC	CTG	CAC	GCT	CTG	CGC	626
I	P	M	S	A	L	P	Y	C	T	W	Q	E	V	Q	A	R	I	V	Q	189
ATC	CCT	ATG	TCT	GCC	CTT	CCG	TAT	TGC	ACG	TGG	CAA	GAA	GTG	CAG	GCC	CGG	ATC	GTG	CAG	686
T	Q	K	E	H	Q	I	C	I	H	K	R	E	L	T	E	L	D	I	Y	209
ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	746
H	R	I	L	R	F	Q	N	Y	M	V	A	L	V	N	K	S	L	L	P	229
CAC	CGC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	806
L	R	F	R	L	P	G	L	G	E	A	V	F	F	T	R	G	L	K	Y	249
CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	866
N	F	E	L	I	L	F	W	G	P	G	S	L	F	L	N	E	W	S	L	269
AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	926
K	A	E	Y	K	R	G	G	Q	R	L	E	L	A	Q	R	L	S	N	R	289
AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	986

Fig. 17I

I	L	W	I	I	G	I	A	N	F	L	L	C	P	L	I	L	I	W	Q	I	309
ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	CTG	TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	1046
L	Y	A	F	F	S	Y	A	E	V	L	L	K	R	E	P	G	A	L	G	A	329
CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	CTG	AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	1106
R	C	W	S	L	Y	G	R	C	Y	L	L	R	H	F	N	E	L	E	H	E	349
CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	CTC	CGC	CAC	TTC	AAC	GAG	CTG	GAG	CAC	GAG	1166
L	Q	S	R	L	N	R	G	Y	K	P	A	S	K	Y	M	N	C	F	L		369
CTG	CAG	TCC	CGC	CTC	AAC	CGT	GGC	TAC	AAG	CCC	GCC	TCC	TCC	AAG	TAC	ATG	AAT	TGC	TTC	TTG	1226
S	P	L	L	T	L	L	A	K	N	G	A	F	F	A	A	G	S	I	L	A	171/361
TCA	CCT	CTT	TTG	ACA	CTG	CTG	GCC	AAG	AAT	GGA	GCC	TTC	TTC	TTC	GCT	GGC	TCC	ATC	CTG	GCT	389
V	L	I	A	L	T	I	Y	D	E	D	V	L	A	V	E	H	V	L	T		409
GTG	CTT	ATT	GCC	CTC	ACC	ATT	TAT	GAC	GAA	GAT	GTG	TTG	GCT	GTG	GAA	CAT	GTG	CTG	ACC		1346
T	V	T	L	L	G	V	T	V	T	V	C	R	S	F	I	P	D	Q	H		429
ACC	GTC	ACA	CTC	CTG	GGG	GTC	ACC	GTG	ACC	GTG	TGC	AGG	TCC	TTT	ATC	CCG	GAC	CAG	CAC		1406
M	V	F	C	P	E	Q	L	L	R	V	I	L	A	H	I	H	Y	M	P		449
ATG	GTG	TTC	TGC	CCT	GAG	CAG	CTG	CTC	CGC	GTG	ATC	CTC	GCT	CAC	ATC	CAC	TAC	ATG	CCT		1466

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Fig. 17J

D	H	W	Q	G	N	A	H	R	S	Q	T	R	D	E	F	A	Q	L	F	469
GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	1526
Q	Y	K	A	V	F	I	L	E	E	L	L	S	P	I	V	T	P	L	I	489
CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	1586
L	I	F	C	L	R	P	R	A	L	E	I	I	D	F	F	R	N	F	T	509
CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	1646
V	E	V	V	G	V	G	D	T	C	S	F	A	Q	M	D	V	R	Q	H	529
GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	TTT	GCT	CAG	ATG	GAT	GTT	CGC	CAG	CAT	1706
G	H	P	Q	W	L	S	A	G	Q	T	E	A	S	V	Y	Q	Q	A	E	549
GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	GAG	GCC	TCA	GTG	TAC	CAG	CAA	GCT	GAG	1766
D	G	K	T	E	L	S	L	M	H	F	A	I	T	N	P	G	W	Q	P	569
GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	GCC	ATC	ACC	AAC	CCT	GGC	TGG	CAG	CCA	1826
P	R	E	S	T	A	F	L	G	F	L	K	E	Q	V	Q	R	D	G	A	589
CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC	AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	1886
A	A	S	L	A	Q	G	G	L	L	P	E	N	A	L	F	T	S	I	Q	609
GCT	GCT	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	1946

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Fig. 17K

S	L	Q	S	E	S	E	P	L	S	L	I	A	N	V	A	G	S	S	629
TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	ATC	GCA	AAT	GTG	GTA	GCT	TCA	TCC	2006
C	R	G	P	P	L	P	R	D	L	Q	G	S	R	R	A	H	S	T	M
TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	GGC	TCC	AGG	CGG	GCT	CAC	AGC	ATG	649
T	G	S	G	V	D	A	R	T	A	S	S	G	S	S	V	W	E	G	Q
ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	ACA	GCC	AGC	TCC	GGG	AGC	AGC	GTG	TGG	GAA	GGA	2126
L	Q	S	L	V	L	S	E	Y	A	S	T	E	M	S	L	H	A	L	Y
CTG	CAG	AGC	CTG	GTG	CTG	TCA	GAA	TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	2186
M	H	Q	L	H	K	Q	Q	A	Q	A	E	P	E	R	H	V	W	H	R
ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	709
R	E	S	D	E	S	G	E	S	A	P	D	E	G	G	E	G	A	R	A
CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GCC	CGG	GCC	729
P	Q	S	I	P	R	S	A	S	Y	P	C	A	A	P	R	P	G	A	P
CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	749
E	T	T	A	L	H	G	G	F	Q	R	R	Y	G	G	I	T	D	P	G
GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	769
																			2426

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Fig. 17L

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Fig. 17M

Fig. 17M

GCTGGAGCGGAGCGCAGGCAATGCTCAGCCCTGGATGTAGCTGAGAGGCTGGGAGAAAGACGACCGCTGGAGACCG 79
AGCGCGTGGGGAAGACCTAGGGGGTGGTGGGGAAGCAGACAGGAGAACTCGAAATCAAGCGCTTACAGATTA 158

TTTTATTTTGTATAGAGAACACGTAGCGACTCCGAAGATCAGCCCCA ATG AAC ATG TCA GTG TTG ACT TTA 8
229

Q E Y E F E K Q F N E N E A I Q W M Q E 28
CAA GAA TAT GAA TTC GAA AAG CAG TTC AAC GAG AAT GAA GCC ATC CAA TGG ATG CAG GAA 289

N W K K S F L F S A L Y A A F I F G G R 48
AAC TGG AAG AAA TCT TTC CTG TTT TCT GCT GCT TAT GCT GCC TTT ATA TTC GGT GGT CGG 349

H L M N K R A K F E L R K P L V L W S L 68
CAC CTA ATG AAT AAA CGA GCA AAG TTT GAA CTG AGG AAG CCA TTA GTG CTC TGG TCT CTG 409

T L A V F S I F G A L R T G A Y M V Y I 88
ACC CTT GCA GTC TTC AGT ATA TTC GGT GCT CTT CGA ACT GGT GCT TAT ATG GTG TAC ATT 469

L M T K G L K Q S V C D Q G F Y N G P V 108
TTG ATG ACC AAA GGC CTG AAG CAG TCA GTT TGT GAC CAG GGT TTT TAC AAT GGA CCT GTC 529

S K F W A Y A F V L S K A P E L G D T I 128
AGC AAA TTC TGG GCT TAT GCA TTT GTG CTA AGC AAA GCA CCC GAA CTA GGA GAT ACA ATA 589

Fig. 18A

F	I	I	L	R	K	Q	K	L	I	F	L	H	W	Y	H	I	T	V	148	
TTC	ATT	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAT	CAC	CAC	ATC	ACT	GTG	649
L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	G	W	F	M	T	168
CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTT	GCC	GGG	GGA	GGT	TGG	TTC	ATG	ACT	709
M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	188
ATG	AAC	TAT	GGC	GTG	CAC	GCC	GTG	ATG	TAC	TCT	TAC	TAT	GCC	TTG	CGG	GCG	GCA	GGT	TTC	769
R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	208
CGA	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	829
G	C	V	V	N	Y	L	V	F	C	W	M	Q	H	D	Q	C	H	S	H	228
GGC	TGT	GTG	GTT	AAC	TAC	CTG	GTC	TTC	TGC	TGG	ATG	CAG	CAT	GAC	CAG	TGT	CAC	TCT	CAC	889
F	Q	N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	248
TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	949
F	F	F	E	A	Y	I	G	K	M	R	K	T	T	K	A	E	*			266
TTT	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	ATG	AGG	AAA	ACA	ACG	AAA	GCT	GAA	TAG			1003
TGTTGGA	ACTGAGGAGGA	AGCCATAGCTCAGGGT	CATCAAGAAAAA	TAATAGACAAA	AGAAAA	ATGGCACAA	AGGAATCAC	1082												
ACGTGGT	GCAGCTAAAA	CAAAACATGAGCA	AAACACAAA	ACC	CAAGGCAGCTTAGGG	ATAATTAGGTTGATT	TAA	1161												

Fig. 18B

CCCAGTAAGTTTATGATCCCTTTTAGGGTGAGGACTCACTGAGTGCACCTCCATCTCCAAGCACCTGCTGCTGGAAGACCC 1240
 CAT'TCCCTCTTTATCTATCAACTCTAGGACAAAGGAGAACAAAAGCAAGCCAGAGAGAGAGACTAATCAAAGGCAA 1319
 ACAAAGGCTATTAAACATAGGAAAAATGTATTTACTAAGTGTACATTTCTCTAAGATGAAAAGATTTT'TACTCTAGA 1398
 AACTGTGCGAGCACAACACACACAATCCCTTTCTAACTTTATGGACACTAAACTGAGCCCAATAGAAAAGACAAAAATGA 1477
 AAGAGACACAGGGTGTATATCTAGAACGATAATGCTTTTGCAGAAACTAAAGCCCTTTTAAAGAAATGCCAGCTGCTGTA 1556
 GACCCCATGAGAAAAAGATGTTTAAATCATCCTTATGAAAAACAGATGTAAACAACATAATTTCAACTAACTTCATCTTCA 1635
 CTGCATAGCCTCAGGCTAGTGAGTTTGCCAAAAACCAAGGGGTGAATACTTCCCCAAGATTTCTCTGGAGGATGGA 1714
 AACAGTGCAGCCAGGTCCCATGGGGCAGCTCCATCCAGAGCATTTCTGATAGTTGAACTGTAAATTTCTACTCTTAA 1793
 GTGAGATATGAAGCATTATCCCTTTTGTTCAGTTGCCCGGCTTTTGAACAGAAAGAGTAAATACAGAAATTGAAAAAGAT 1872
 AAACACTCAACCCAAACAATGTGAAAAACGGGTTCTGTAGTATTTGTAAAAAGGCCCGCCAGGACCACCTGTGAGCTGGA 1951
 AAAGGGAGAAAGCAGTGGGAAAAGAGGTGAGCCGAAGATCAATTCGACAGACAGACGGTGTGTATGCCCCCTCCCTGTT 2030
 TGACTTCACACACACTCATAACTTTCCAAATGAAACCCACAGTATAGCGCATATTTTCGATATTTTGTGAAATTCCAA 2109
 AAGGAAATCACAGGGCTGTTTCGAAATATTTGGGGGAACACACTGTGTTTCTGTCATCATCTGCATTTGCTCCCCAAGCAAATGT 2188
 AGAGGTGTTTAAAGGGCCCTCTGCTGGCTGAGTGGCAA TACTACAACAACCTTCAAGGCAAGTTTGGCTGAAAAACAGTT 2267
 GACAAACAAGGGCCCCATACACTTATCCCTCAAATTTTAAAGTGATATGAAATACTTGTCACTGCTTTTGGCCAAATCAG 2346
 AAGATATTCAATCCCTGCTTCAAGTCAGCTTCAGAAATGTTTAAAGGGACTTTAGCTCTGGAACCTCAAAATCAATTTAT 2425
 TAAAGAGCCATATTCTTTAAAAAAAAGCTGGATAATATTCTCTGTAAATATTTCAGTCTTTTACAAGCCAAATACATG 2504
 TGTCAAATGTTTCTAGTATTTCAAAGAAGCAATTATGTAAAGTTGTTTCAATGTGACATAAATAGTATTATAATTGGTTAAG 2583
 TAGCTTAATGATTAGGCAAACTAGATGAAAAGATTAGGGCTTCCACACTGCATAGATTACACGCACATAGCCACGCAT 2662
 ACACACACAGACACACAGATGTGGGGTACACTGAACCTTCAAAGCCCAAATGAATAGAAAACACATTTTCTGGCTAGCAGA 2741
 AAAAAACAAAACAAAACCTGTGTGTTTCTCTTTCTTGCTTTTGAGAGTGTACAGTAAAAAGGGATTTTTCGAATATTTTTA 2820
 TATTATTTTAGCTTTAATTGTGCTGTCGTTTCATGAAAACAGAGCTGCTCTGCTTTTCTGTGAGAGATGGCAAGGCTTTT 2899
 TCAGCATCTCGTTTATGTGTGGAATTTAAAAAGAAATAAAGTTTATTCATTTCTGTGTGAAAAAATAAAAAA 2978
 AAAAAAATAA

Fig. 18C

L	K	Q	S	V	C	D	Q	S	F	Y	N	G	P	V	S	K	F	W	19	
GC	CTG	AAG	CAG	TCA	GTT	TGT	GAC	CAG	AGT	TTT	TAC	AAT	GGA	CCT	GTC	AGC	AAA	TTC	TGG	59
A	Y	A	F	V	L	S	K	A	P	E	L	G	D	T	I	F	I	I	L	39
GCT	TAT	GCA	TTT	GTG	CTC	AGC	AAA	GCA	CCC	GAA	CTA	GGT	GAC	ACG	ATA	TTC	ATC	ATT	CTG	119
R	K	Q	K	L	I	F	L	H	W	Y	H	H	I	T	V	L	L	Y	S	59
AGG	AAA	CAG	AAA	CTG	ATC	TTC	CTG	CAC	TGG	TAC	CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCC	179
W	Y	S	Y	K	D	M	V	A	G	G	G	W	F	M	T	M	N	Y	G	79
TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTC	GCT	GGG	GGT	GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	239
V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	R	V	S	R	99
GTG	CAT	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	CGG	GCT	GCG	GGT	TTC	CGA	GTC	TCC	CGG	299
K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	G	C	V	I	119
AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	359
N	Y	L	V	F	N	W	M	Q	H	D	N	D	Q	C	Y	S	H	F	Q	139
AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	AAC	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	419
N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	F	F	159
AAC	ATC	TTC	TGG	TCC	TCG	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	TTC	TTC	479

Fig. 18E

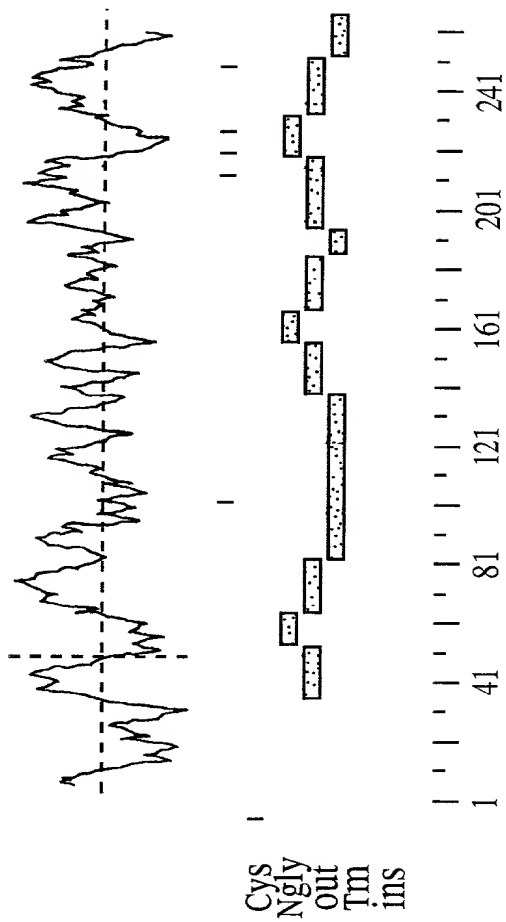


FIG. 18D

F E A Y I G K V K A T K A E *

TTT GAG GCC TAC ATC GGC AAA GTG AAG AAA GCC ACG AAG GCT GAG TAG 175
527

TGTCAGGGCTGAGGAGGAAGTCATAGCTCAGGGTCATCACGAAAAATAATCGACAAAAAATGGCACAAAGGAATCC 606
CATATGGTGCAGCTAAACAAACAAACATCCGTATGAGCAGGCACGAGGCCAAGGCAGCTTGGGACTGAAGATTAG 685
GTTGTAAGTTTATGATCCTTTCTGGGTGAGGACTCGCTGAGTGCACCTTTATCTCAAAGCACGGCTGCTGAGGGGACC 764
CCTTCCCTCTGGCCCTGTCAACTCTAGAAACACACTAGATGCAAAAGGCAGCCACGGGCAAGAGATTGGGCAGAGATTAGT 843
GGACGGCCAGCAAAACACTGCAGGAAGCAGGTGGGGGAGGAATCTACTCAGCCCTTTTGTGTTTGTGTTTGTGTTT 922
GTTTCTCTAAGGATAAAGGAGTTTCCCCTTTTCAAACGATGTAGCACACACACACACACACACACACACACA 1001
CACACACACACACGCAATCTTTTCAAACGAAACAGAGCTAAAGAAAGATAAACAATGGAGAGACAGGTTTCTAT 1080
CTGGGACAGCAATGCTTTTGCAAAAGGCTAGGCCCTTTTAAAGAAAGGTGAGCTTGTAATCTCTTGATAAAGATGCTT 1159
AATTATTTTACTGCAACTGAAAGTAAGAGGTAGAGCCCTTTCCCCTTCTGCACAGCCCTCAGGGCTTGATGTTCTCTA 1238
CAACCAACACACAGGACAGTACTTCCCCTATGATATCTTACTGGGAGAAAGAACCCCTGTAGTTGAAACACACAC 1317
TGACAACTGTTATTTCTGCTCTCCGACGAGAAATCAAGCATCCGTTGTTGCCCCAAACTTTAGGACGGAGGAGT 1396
AAATGCAGAACTGAAAGGGAAGAGCTCAGCTGGCTGGCTTGAAAAATGGAGTCTTGTAACCATGTGTAACAAATGCCAGC 1475
CCATCGTCCCTGGAGCTGAACAGGGAGGAAGGCTATGGGCAGAGACTAGAGCCGATTCTCAATGTGCAGACAGCG 1554
TGTTCCGCTCCCTCCCTGTTTCGACCTCACACATAATCCCTGGCTTCTAAATGAGGCCCTGTGACACACTCTGTGCTTTC 1633
TATATTTTGTGACTTTCAAACACAGATCTGCAGGGCTCTGCCCTGATTTGGGGTAAACACTGTGTTTCTGCAGCCTCTG 1712
CATTTGCTCCCTTCAGCAGTGCAGAGGCTTGAGAAAGTGCCCTCTGCTGGCTTAGTGAGAAGCTTCAACAAACACTTCAC 1791
AGTAGGTTGAAATAACTGACCACTAAGGGCTGCGGAGATTAAACCCCTAAGTCTAAGTGTGTCAAAACACCTGACATA 1870
TATTTGACCAAAATCAGAAAGAGAGAGAAACCTCTATGCTTCAAGTAAGCGTCAATAAATTTTTTAAGTGACTTTCACCTG 1949
AGAACTCAGAAAGTCAATGTATTAAAGGCCATATTTCTGAAAGAAAGAAAGAGAAAGAAAGAAAAA 2028
AAAA 2032

Fig. 18F

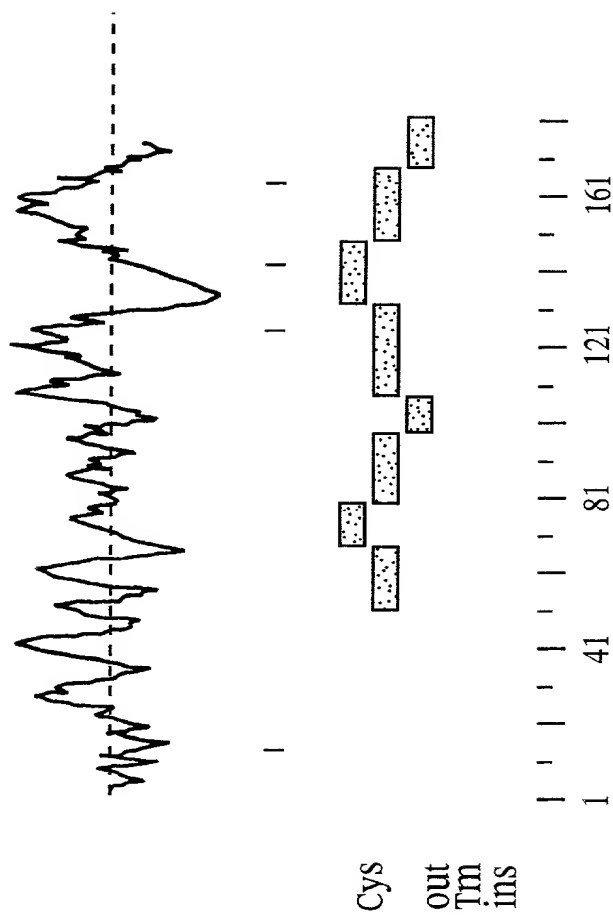


FIG. 186

[illegible]

Fig. 18H

human	ATGAACATGTCAGTGTGACTTTACAAGAATATGAATTCGAAAAGCAGTTCACGAGAATGAAGCCATCC	10	20	30	40	50	60	70
murine	-----							
human	AATGGATGCAGGAAACTGGAAGAAATCTTTCCTGTTTTCTGCTCTGTATGCTGCCCTTTATATTCGGTGG	80	90	100	110	120	130	140
murine	-----							
human	TCGGCACCTAATGAATAAACGAGCAAAGTTTGAACTGAGGAAGCCATTAGTGCTCTGGTCTCTGACCCCTT	150	160	170	180	190	200	210
murine	-----							
human	GCAGTCTTCAGTATATTCCGGTGCTCTTCGAACTGGTGCTTATATGTTGATGACCAAAGGCC	220	230	240	250	260	270	280
murine	-----							

Fig. 181

human	290	300	310	320	330	340	350
	TGAAGCAGTCAGTTTGTGACCCAGGGTTTTTACAATGGACCTGTCAGCAAATTCCTGGGCTTATGCATTGTG						
	::						
murine	TGAAGCAGTCAGTTTGTGACCCAGAGTTTTTACAATGGACCTGTCAGCAAATTCCTGGGCTTATGCATTGTG						
	10	20	30	40	50	60	70
human	360	370	380	390	400	410	420
	GCTAAGCAAAGCACCCGAACTAGGAGATACAAATATTCATTATCTGAGGAAGCAGAAAGCTGATCTTCCTG						
	::: ::						
murine	GCTCAGCAAAGCACCCGAACTAGGTGACACGATATTCATCATCTGAGGAAAACAGAAACTGATCTTCCTG						
	80	90	100	110	120	130	140
human	430	440	450	460	470	480	490
	CACTGGTATCACCCACATCACTGTGCTCCTGTACTCTTGGTACTCCTACAAAGACATGGTTCCTGGGGGAG						
	::::::::: :: :: ::::::::::						
murine	CACTGGTACCACCCACATCACTGTGCTCCTGTACTCCTGGTACTCCTACAAAGACATGGTCGTGGGGTG						
	150	160	170	180	190	200	210
human	500	510	520	530	540	550	560
	GTTGGTTCACTAGTATGAACATATGGCGTGACGCCGTGATGTACTCTTACTATGCCCTTGCGGCGGCAGG						
	::						
murine	GTTGGTTCACTAGTATGAACATATGGCGTGACGCCGTGATGTACTCTTACTACGCCCTTGCGGGCTGCCGG						
	220	230	240	250	260	270	280

Fig. 18J

	570	580	590	600	610	620	630
human	TTTCCGAGTCTCCCGGAAGTTTGCCATGTTCA	CACCTTG	TCCAGATCA	CTCAGATG	CTGATGGG	CTGT	
	290	300	310	320	330	340	350
murine	TTTCCGAGTCTCCCGGAAGTTTGCCATGTTCA	CACCTTG	TCCAGATCA	CTCAGATG	CTGATGGG	CTGT	
	640	650	660	670	680	690	
human	GTGGTTAACTACCTGGTCTTCTGCTGGATGC	AGATGAC	-----	CAGTGTCA	CTCTCA	CTTTCAGAA	CA
	360	370	380	390	400	410	420
murine	GTCATTAACTACCTGGTCTTCAACTGGATGC	AGATGAC	AAACGAC	GTGCTACT	CTCCACTT	TCAGAA	CA
	700	710	720	730	740	750	760
human	TCTTCTGGTCCCTCACTCATGTACCTCAGCT	ACCTTGT	GTCTCTTCTGCC	ATTCTTCT	TGAGGC	CTACAT	
	430	440	450	460	470	480	490
murine	TCTTCTGGTCCCTCGCTCATGTACCTCAGCT	ACCTTGT	GTCTCTTCTGCC	ATTCTTCT	TGAGGC	CTACAT	
	770	780	790				
human	CGGCAAAATGAGGAAAACAAACGAAAGCT	GAA					
	500	510	520				
murine	CGGCAAAAGTGAAGAAAAGCCACGAAGGCT	GAG					

Fig. 18K

Fig. 18L

Fig. 18M

```

270      280      290      300      310      320
I400 ATTTTGATGACCAAAGGCCTGAAGCAGTCAGTTTG--TGACCAGGGTTTTTACAATGGAC-CTGTCAGCA
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 GTGATGTTTACAGTGGGCCTCAAGCAAACCGTGTGCTTTGCCA--TCTACACGGATGACGCCGTAGTCA
    280      290      300      310      320      330      340

330      340      350      360      370      380      390
I400 AATTCTGGCCTTATGCATTTGTGCTAAGCAAAGCACCCGAACTAGGAGATACAATATTCAATTATTCTGAG
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 GATTCCTGGTCCTTTCTCTCTTCTTCTCTCAGCAAAGGTTGTTGAAGTGGGAGACACGGCCTTCATCATCCTGCG
    350      360      370      380      390      400      410

400      410      420      430      440      450      460
I400 GAAGCAGAAGCTGATCTTCCCTGCACCTGGTATCACCCACATCACTGTGCTCCTGTACTCTTGGTACTCCTAC
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 TAAGCGTCCACTCATCTTTGTCCACTGGTACCACCCACAGCACAGTGCTACTGTTTACAAAGCTTTGGATAC
    420      430      440      450      460      470      480

470      480      490      500      510      520      530
I400 AAAGACATGGTTGCCGG-GGGAGGTTGGTTCATGACTATGAACCTATGGCGTGCACGCCGTGATGTACTCT
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 AAGAACAAAGT-GCCTTCGGGTGGCTGGTTCATGACCATGAACTTTGGCGTCCATTCTGTCTATGTACACT
    490      500      510      520      530      540      550

```

Fig. 18N

Figure 180

```

540      550      560      570      580      590      600
I400 TACTATGCCCTTGC GGCGGCAGGTTTCCGAGTCTCCCGAAGTTTGCC--ATGTTTCATCACCTTGTCC--
      ::::: :: ::::: :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 TACTACACTATGAAGGCTGCCAAA--CTGAAGCATCCCTAATCTTCTCCCCATGGTCAATCACCCAG--CCTG
      560      570      580      590      600      610

610      620      630      640      650      660      670
I400 CAGATCACT-CAGATGCTGATGGGCTGTGTGTTAACTACCTGGTCTTCTGCTGGATGCAGCATGACCAG
      ::::: :: ::::: :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 CAGAT-TCTGCAGATGGTTCTGCGGCACCATCTTTTGGCATACTGAATTACATCTGGAGGCAGGAGAAAAGGA
      620      630      640      650      660      670      680

680      690      700      710      720      730      740
I400 TGTCACTCTCACTTTCAGAAACA--TCTTCTGGTCCCTCACTCATGTACCTCAGCTACCTTGTGCTCTTCTG
      :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 TGCCACACACA-ACAA-CGGAACACTTCTTCTGCTCTTTTATGCTATATGGGACCTATTTTCATCCCTATTTCGC
      690      700      710      720      730      740      750

750      760      770      780      790
I400 CCATTCTTCTTTGAGGCCCTACATCGG--CAAAATGAGGAAACAAC-GAAAGCTGAA
      :: ::::: . ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 TCACTTCTTCCACCGAGCCTACCTCAGGCCCAAGGGCAAAGTTGCATCCCAAGAGCC-AA
      760      770      780      790      800      810

```

Fig. 180

L	G	D	T	I	F	I	I	L	R	K	Q	K	L	I	F	L	H	W	Y	20
CTA	GGT	GAT	ACG	ATA	TTC	ATC	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAC	60
H	H	I	T	V	L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	40
CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTA	GCT	GGG	GGT	120
G	W	F	M	T	M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	60
GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	GTA	CAC	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	180
R	A	A	G	F	R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	80
CGG	GCT	GCG	GGT	TTC	CGG	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACG	TTG	TCC	CAG	ATC	240
T	Q	M	L	M	G	C	V	I	N	Y	L	V	F	N	W	M	Q	H	D	100
ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	300
N	D	Q	C	Y	S	H	F	Q	N	I	F	W	S	S	L	M	Y	L	S	120
AAT	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	360
Y	L	L	L	F	C	H	F	F	F	E	A	Y	I	G	K	V	K	K	A	140
TAC	CTT	CTG	CTC	TTC	TGC	CAT	TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCG	420
T	K	A	E	*																145
ACG	AAG	GCC	GAG	TAG																435

Fig. 18P

Fig. 18Q

Fig. 18R

GTCGACCCACGCGTCCGGGAGCGGGCTAAGAGTCCCGCACCGCCTCACAACCTGGGAACCGGAGAGTAGGGCCGTC	79
GGCTGGCAAGAACCCGCGTCCCTCGGCAAGGGCCATCCGGTGCCACCCCATGTCCGCACTAGACAGAAGAGGGTGA	158
<div> <div>M</div> <div>T</div> <div>W</div> <div>L</div> <div>V</div> </div>	
GTCCTGAACCTGCACAGAGCTGCTCTGTACTGTCCCTGGTGGTCCCGCC ATG ACC TGG TTG GTG	5 229
L L G T L L C M L R V G L G T P D S E G	25
CTG CTG GGG ACA CTG CTC TGC ATG CTG CGC GTT GGG TTA GGC ACC CCG GAC TCC GAG GGT	289
F P P R A L H N C P Y K C I C A A D L L	45
TTC CCG CCC CGT GCG CTC CAC AAC TGC CCC TAC AAA TGT ATC TGC GCT GCC GAC CTG CTA	349
S C T G L G L Q D V P A E L P A A T A D	65
AGC TGC ACT GGC CTA GGG CTG CAG GAC GAC GTG CCA GCC GAG TTA CCT GCC GCT ACT GCG GAC	409
L D L S H N A L Q R L R P G W L A P L F	85
CTC GAC CTG AGC CAC AAC GCG CTC CAG CGC CTG CGC CCC GGC TGG TGG GCG CCC CTC TTC	469
Q L R A L H L D H N E L D A L G R G V F	105
CAG CTG CGC GCC CTG CAC CTA GAC CAC AAC GAA CTA GAT GCG CTG GGT CGC GGC GTC TTC	529
V N A S G L R L L D L S S N T L R A L G	125
GTC AAC GCC AGC GGC CTG AGG CTG CTC GAT CTA TCA TCT AAC ACG TTG CGG GCG CTT GGC	589

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Fig. 19A

R	H	D	L	D	G	L	G	A	L	E	K	L	L	L	F	N	N	R	L	145
CGC	CAC	GAC	CTC	GAC	GGG	CTG	GGG	GCG	CTG	GAG	AAG	CTG	CTT	CTG	TTC	AAT	AAC	CGC	TTG	649
V	H	L	D	E	H	A	F	H	G	L	R	A	L	S	H	L	Y	L	G	165
GTG	CAC	TTG	GAC	GAG	CAT	GCC	TTC	CAC	GGC	CTG	CGC	GCG	CTC	AGC	CAT	CTC	TAC	CTG	GGC	709
C	N	E	L	A	S	F	S	F	D	H	L	H	G	L	S	A	T	H	L	185
TGC	AAC	GAA	CTC	GCC	TCG	TTC	TCC	TTC	GAC	CAC	CTG	CAC	GGT	CTG	AGC	GCC	ACC	CAC	CTG	769
L	T	L	D	L	S	S	N	R	L	G	H	I	S	V	P	E	L	A	A	205
CTT	ACT	CTG	GAC	CTC	TCC	TCC	AAC	CGG	CTG	GGA	CAC	ATC	TCC	GTA	CCT	GAG	CTG	GCC	GCG	829
L	P	A	F	L	K	N	G	L	Y	L	H	N	N	P	L	P	C	D	C	225
CTG	CCG	GCC	TTC	CTC	AAG	AAC	GGC	CTC	TAC	TTG	CAC	AAC	AAC	CCT	TTG	CCT	TGC	GAC	TGC	889
R	L	Y	H	L	L	Q	R	W	H	Q	R	G	L	S	A	V	R	D	F	245
CGC	CTC	TAC	CAC	CTG	CTA	CAG	CGC	TGG	CAC	CAG	CGG	GGC	CTG	AGC	GCC	GTG	CGC	GAC	TTT	949
A	R	E	Y	V	C	L	A	F	K	V	P	A	S	R	V	R	F	F	Q	265
GCG	CGC	GAG	TAC	GTA	TGC	TTG	GCC	TTC	AAG	GTA	CCC	GCG	TCC	CGC	GTG	CGC	TTC	TTC	CAG	1009
H	S	R	V	F	E	N	C	S	S	A	P	A	L	G	L	K	R	P	E	285
CAC	AGC	CGC	GTC	TTT	GAG	AAC	TGC	TCG	TCG	GCC	CCA	GCT	CTT	GGC	CTA	AAG	CGG	CCG	GAA	1069

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Fig. 19B

E H L Y A L V G R S L R L Y C N T S V P 305
 GAG CAC CTG TAC GCG CTG GGT TCC CTG AGG CTT TAC TGC AAC ACC AGC GTC CCG 1129

 A M R I A W V S P Q Q CAG CAG GAG CTT CTC AGG GCG CCA GGA TCC CGC 1189
 GCC ATG CGC ATT GCC TGG GTT TCG CCG CAG CAG CAG CTT CTC AGG GCG CCA GGA TCC CGC 1189

 D G S I A V L A D G S L A I G N V Q E Q 345
 GAT GGC AGC ATC GCG GTG CTG GGC GAC GGC AGC TTG GCC ATA GGC AAC GTA CAG GAG CAG 1249

 H A G L F V C L A T G P R L H H N Q T H 365
 CAT GCG GGA CTC TTC GTG TGC CTG GGC ACT GGC CCC CGC CTG CAC CAC AAC CAG ACG CAC 1309

 E Y N V S V H F P R P E P E A F N T G F 385
 GAG TAC AAC GTG AGC GTG CAC TTT CCG CGC CCA GAG CCC GAG GCT TTC AAC ACA GGC TTC 1369

 T T L L G C A V G L V L V L L Y L F A P 405
 ACC ACA CTG CTG GGC TGT GCC GTG GGC CTT GTG CTC GTG CTG CTC TAC CTG TTC GCC CCA 1429

 P C R C C R A C P L P P L A P N T Q P 425
 CCC TGC CGC TGC TGC CGC CGT GCC TGC CCG CTG CCG CCG CTG GCC CCA AAC ACC CAG CCC 1489

 A P R A E P H K S S V L S T T P P D A P 445
 GCT CCA AGA GCT GAG CCG CAC AAG TCC TCA GTA CTC AGC ACC ACA CCG CCA GAC GCA CCC 1549

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Fig. 19C

S	P	Q	G	Q	A	S	T	S	T	*												
AGC	CCG	CAA	GGC	CAA	GCG	TCC	ACA	AGC	ACG	TAG	456											
											1582											
TCT	TTCT	GGAGCC	AGG	CCGG	AGGG	CCCTCA	ATGG	CCCG	CGTGC	AGCTGG	CAGTAG	CTGAG	GAATTC	GATCTCT	ACAACC	1661						
CTG	AGG	CCTGC	AGCTGA	AGGCTGG	CTCTG	AGTCCG	CCAGCTCC	ATAGG	CTCCG	AGGTC	CCATG	ACAACC	TAG	ACTGC	1740							
CAG	GGCT	CCCC	ACCC	AGG	CCCC	ACCCCTCT	TGCTG	CTG	CTCC	CTGCTT	CGGTCC	AGAGAA	CTGG	CAGATA	CT	1819						
GGT	GGAA	GC	ACTGT	GCCTGG	CCCC	AGCTTCC	TGTAT	GGCC	TCGAA	ACACA	ATGG	GCCTT	CTCG	CTCA	CTGG	TAGA	1898					
GAC	AGG	GT	TG	GGTCCCC	AACTGC	CTTCT	GTCTG	CTCCCC	TGC	ACAGG	ACCC	AAAGG	CCCC	AGG	CCCC	TGCAAG	GTG	1977				
CTA	GT	TCC	TG	CTTT	CCCGG	ACTTCC	TAGT	GCCCC	AAATG	CCCC	CTGTG	AGGCTG	AGAG	ACCC	AGG	CCCC	TGTG	GGCTTT	CA	2056		
AC	AG	CAC	AG	CTGT	GGA	AGTGG	CTGT	GTCTT	CTAC	AGCC	TGTG	GAA	GAAC	CCCC	TGTAG	CAGAG	CCCTCC	CCATCC	ACCC	2135		
TC	AGG	GGCTG	AGG	CAG	CTCT	CAGG	AGTGG	TGCTCA	AGAG	CTGAC	GCAG	GGCC	ACCT	CCCC	TTCC	CAAG	GGGTGG	GAG	2214			
GG	AGT	GG	CCCC	CAG	GGAA	AGAGG	CGGCTCT	GAA	GAAGAT	CTCG	CCCC	CAC	CCCC	CAG	GACAG	AAAG	AGAA	CAAGC	2293			
CCG	CC	CT	GT	GAA	ATGG	GA	CTCC	CTC	ATCC	ACCA	CAAC	CCCA	CTCT	CTG	AAAG	CTTCA	CA	AACTTCA	CGC	AGAG	TCC	2372
GGT	GC	AG	CC	AG	GC	AGG	CTCCT	CAAG	AGGTT	CCCTG	GTG	GTCT	G	CCCTA	AG	CCCC	AGCC	AGAG	GGCC	CTG	CTC	2451

Fig. 19D

TCTCTGGCCTGGGGCATCCACCCGTTGTTCTGAAGCAGAGCCCATTTCTGTGGGCTCACAAGACACAGTGAAGGGGATC 2530
 ATGGCCTGCACCCCTGCTTTTCAGCAGTAAAAAGCCCGAAAGCCTGGCGAGCATGGCCGAGCTGGGAGGGCCGAGCCG 2609
 GAACTCCACGTCCTCGAGAGCAGGAGCCCTCTTAAGGGCTGGCACTGGTCTCAGCCCTAATGGCTGAGGCGGTACCCCTGG 2688
 CTTCATATGCATCTCACTGCTCCCACCTGCAGGGGGCAGGGAAGGGGGTCTGGGAGCCCTTCATGTGTGGGGCCGAG 2767
 CTGGGGGCCCCCATGGCCATCCCTGGACCTCGCTGCTCCAGAGTTTAATAAAGGTAGCACATGCTTATTGCTAGAAAAAA 2846
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2895

Fig. 19E



FIG. 19F

[illegible]

Fig. 19G

```

270      280      290      300      310      320
H SRVFENCSSA-PALGLKRPEEHLIALVGRSL-----RLYCNTSV-PAMRIAWVSPQQELLRAPGSRDGS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
P DITASGCRDLCRVLQAKETLKEI-SLAGNKLGDGARGLLCESLLQPGCQLESILWVKSCSLTAACQHVSL
270      280      290      300      310      320      330

330      340      350      360      370      380      390
H AVLADGSLAIGNVQEQHAGLFVCLATGPRLHHNQTHEYNVSVHFFRPEPEAFNTGFTLLGCAVGLVLVL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
P MLTQNKHL-----LEIQLSNKLGDSDGIQELCQALSQPGTTLRVLCIGDCEVTNSGCSSLAS--LLANRS
340      350      360      370      380      390

400      410      420      430      440      450
H LYLFAPPCRRACPLPPLAPNTQPAPRAEPHK-SSVLSTTPPDAPSPQQASTS-----T
: . . . . : : : : : : : : : : : : : : : : : : : : : : : :
P LRELDLSNNCVGDPGVQLQLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVIS
400      410      420      430      440      450

```

Fig. 19H

Sequence

ccg ttt ctc ttt aac cac ttg cac ggt ctg ggg tta acc cgc ctg cgg	48
Pro Phe Leu Phe Asn His Leu His Gly Leu Thr Arg Leu Arg	
1 5 10 15	
act ctg gac ctc tcc tcc aac tgg ctg aaa cat atc tcc atc cct gag	96
Thr Leu Asp Leu Ser Ser Ser Asn Trp Leu Lys His Ile Ser Ile Pro Glu	
20 25 30	
ttg gct gca ctg cca act tat ctc aag aac agg agc ctc tac ctg cac aac	144
Leu Ala Ala Leu Pro Thr Tyr Leu Lys Asn Arg Leu Tyr Leu His Asn	
35 40 45	
aac ccg ctg ccc tgt gac tgc agc ctc tac cac ctg ctc cgg cgc tgg	192
Asn Pro Leu Pro Cys Asp Cys Ser Leu Tyr His Leu Leu Arg Arg Trp	
50 55 60	
cac cag cgg ggc ctg agt gcc ctg cat gat ttt gaa cgc gag tac aca	240
His Gln Arg Gly Leu Ser Ala Leu His Asp Phe Glu Arg Glu Tyr Thr	
65 70 75 80	
tgc ttg gtc ttt aag gtg tca gag tcc cga gtg cgc ttt ttt gag cac	288
Cys Leu Val Phe Lys Val Ser Glu Ser Arg Val Arg Phe Phe Glu His	
85 90 95	
agc cgg gtc ttc aag aac tgc tct gtg gct gca gct cca ggc tta gag	336
Ser Arg Val Phe Lys Asn Cys Ser Val Ala Ala Ala Pro Gly Leu Glu	
100 105 110	

Fig. 19I

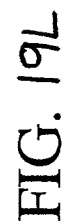
Letter "G" repeated

ctg cct gaa gag gag cag ctg cac gcg cag gtg ggc cag tcc ctg agg ctc Leu Pro Glu Glu Gln Leu His Ala Gln Val Gly Gln Ser Leu Arg Leu	115 120 125	384
ttc tgc aac acc agt gtg cct gcc act cgg gtg gcc tgg gtc tcc ccg Phe Cys Asn Thr Ser Val Pro Ala Thr Arg Val Ala Trp Val Ser Pro	130 135 140	432
aag aat gag ctg ctt gtg gcg cca gcc tct cag gat ggt agc atc gct Lys Asn Glu Leu Leu Val Ala Pro Ala Ser Gln Asp Gly Ser Ile Ala	145 150 155 160	480
gtg ttg gct gat ggc agc tta gcc ata ggc agg gtg caa gag cag cac Val Leu Ala Asp Gly Ser Leu Ala Ile Gly Arg Val Gln Glu Gln His	165 170 175	528
gca ggc gtc ttt gtg tgc ctg gcc agt ggg ccc cgc ctg cac cac aac Ala Gly Val Phe Val Cys Leu Ala Ser Gly Pro Arg Leu His His Asn	180 185 190	576
cag aca ctt gag tac aat gtg agt gtg caa aag gct cgc ccc gag cca Gln Thr Leu Glu Tyr Asn Val Ser Val Gln Lys Ala Arg Pro Glu Pro	195 200 205	624
gag act ttc aac aca ggc ttt acc acc ctg ggc tgt att gtg ggc Glu Thr Phe Asn Thr Gly Phe Thr Thr Leu Leu Cys Ile Val Gly	210 215 220	672

Fig. 19J

ctg gtg ctg gtg ttg ctg tac ttg ttt gca cca ccc tgt cgt ggc tgc Leu Val Leu Val Leu Leu Tyr Leu Phe Ala Pro Pro Cys Arg Gly Cys 225 230 235 240 245	720
tgt cac tgc tgt cag cgg gcc tgc tgc aac cgt tgc tgg ccc cgg gca Cys His Cys Cys Gln Arg Ala Cys Arg Asn Arg Cys Trp Pro Arg Ala 245 250 255	768
tcc agt cca ctc cag gag ctg agc gca cag tcc tcc atg ctt agc act Ser Ser Pro Leu Gln Glu Leu Ser Ala Gln Ser Ser Met Leu Ser Thr 260 265	816
acg cca cca gat gca ccc agc cgc aag gcc agt gtc cac aag cat gtg Thr Pro Pro Asp Ala Pro Ser Arg Lys Ala Ser Val His Lys His Val 275 280 285	864
gtc ttc ctg gag ccg ggc aag aag ggc ctc aat ggc cgt gtg cag ctc Val Phe Leu Glu Pro Gly Lys Lys Gly Leu Asn Asn Gly Arg Val Gln Leu 290 295 300	912
gca gta cct cca gac tcc gat ctg tgc aac ccc atg ggc ttg caa ctc Ala Val Pro Pro Asp Ser Asp Leu Cys Asn Pro Met Gly Leu Gln Ieu 305 310 315 320	960
aa	962

Fig. 19K



GTCGACCCACGCGTCCGGCGAACCCAGCGTCCGCCGAC	ATG	GCC	TGG	ACC	AAG	TAC	CAG	Q	L	F	L	10
A	G	L	M	L	V	T	G	S	I	N	T	69
GCC	GGG	CTC	ATG	CTT	GTT	ACC	GGC	TCC	ATC	AAC	ACG	
F	M	A	E	G	C	G	G	S	K	E	H	30
TTC	ATG	GCC	GAG	GGC	TGT	GGA	GGG	AGC	AAG	GAG	CAC	129
A	V	G	M	F	L	G	E	F	S	C	L	50
GCA	GTG	GGC	ATG	TTC	CTG	GGA	GAA	TTC	TCC	TGC	CTG	189
R	A	A	G	Q	S	D	S	S	V	D	P	70
AGA	GCT	GCA	GGG	CAA	TCA	GAC	TCC	AGC	GTA	GAC	CCC	249
F	L	P	P	A	L	C	D	M	T	G	T	90
TTC	CTG	CCC	CCA	GCG	CTC	TGT	GAC	ATG	ACA	GGG	ACC	309
M	T	S	A	S	S	F	Q	M	L	R	G	110
ATG	ACC	AGT	GCC	TCC	AGC	TTC	CAG	ATG	CTG	CGG	GGT	369
F	S	V	A	F	L	G	R	L	L	V	L	130
TTC	TCG	GTG	GCC	TTC	CTG	GGC	CGG	AGG	CTG	GTG	CTG	429
A	G	L	M	L	V	T	G	S	I	N	T	150
GCC	GGG	CTC	ATG	CTT	GTT	ACC	GGC	TCC	ATC	AAC	ACG	489
F	M	A	E	G	C	G	G	S	K	E	H	30
TTC	ATG	GCC	GAG	GGC	TGT	GGA	GGG	AGC	AAG	GAG	CAC	129
A	V	G	M	F	L	G	E	F	S	C	L	50
GCA	GTG	GGC	ATG	TTC	CTG	GGA	GAA	TTC	TCC	TGC	CTG	189
R	A	A	G	Q	S	D	S	S	V	D	P	70
AGA	GCT	GCA	GGG	CAA	TCA	GAC	TCC	AGC	GTA	GAC	CCC	249
F	L	P	P	A	L	C	D	M	T	G	T	90
TTC	CTG	CCC	CCA	GCG	CTC	TGT	GAC	ATG	ACA	GGG	ACC	309
M	T	S	A	S	S	F	Q	M	L	R	G	110
ATG	ACC	AGT	GCC	TCC	AGC	TTC	CAG	ATG	CTG	CGG	GGT	369
F	S	V	A	F	L	G	R	L	L	V	L	130
TTC	TCG	GTG	GCC	TTC	CTG	GGC	CGG	AGG	CTG	GTG	CTG	429
A	G	L	M	L	V	T	G	S	I	N	T	150
GCC	GGG	CTC	ATG	CTT	GTT	ACC	GGC	TCC	ATC	AAC	ACG	489
F	M	A	E	G	C	G	G	S	K	E	H	30
TTC	ATG	GCC	GAG	GGC	TGT	GGA	GGG	AGC	AAG	GAG	CAC	129
A	V	G	M	F	L	G	E	F	S	C	L	50
GCA	GTG	GGC	ATG	TTC	CTG	GGA	GAA	TTC	TCC	TGC	CTG	189
R	A	A	G	Q	S	D	S	S	V	D	P	70
AGA	GCT	GCA	GGG	CAA	TCA	GAC	TCC	AGC	GTA	GAC	CCC	249
F	L	P	P	A	L	C	D	M	T	G	T	90
TTC	CTG	CCC	CCA	GCG	CTC	TGT	GAC	ATG	ACA	GGG	ACC	309
M	T	S	A	S	S	F	Q	M	L	R	G	110
ATG	ACC	AGT	GCC	TCC	AGC	TTC	CAG	ATG	CTG	CGG	GGT	369
F	S	V	A	F	L	G	R	L	L	V	L	130
TTC	TCG	GTG	GCC	TTC	CTG	GGC	CGG	AGG	CTG	GTG	CTG	429
A	G	L	M	L	V	T	G	S	I	N	T	150
GCC	GGG	CTC	ATG	CTT	GTT	ACC	GGC	TCC	ATC	AAC	ACG	489
F	M	A	E	G	C	G	G	S	K	E	H	30
TTC	ATG	GCC	GAG	GGC	TGT	GGA	GGG	AGC	AAG	GAG	CAC	129
A	V	G	M	F	L	G	E	F	S	C	L	50
GCA	GTG	GGC	ATG	TTC	CTG	GGA	GAA	TTC	TCC	TGC	CTG	189
R	A	A	G	Q	S	D	S	S	V	D	P	70
AGA	GCT	GCA	GGG	CAA	TCA	GAC	TCC	AGC	G			

Fig. 20A

T	I	A	G	L	V	V	G	L	A	D	L	L	S	K	H	D	S	Q	170	
ACC	ATC	GCG	GGG	CTG	GTG	GTC	GTG	GGC	CTG	GCT	GAC	CTC	CTG	AGC	AAG	CAC	GAC	AGT	CAG	549
H	K	L	S	E	V	I	T	G	D	L	L	I	I	M	A	Q	I	I	V	190
CAC	AAG	CTC	AGC	GAA	GTG	ATC	ACA	GGG	GAC	CTG	TTG	ATC	ATC	ATG	GCC	CAG	ATC	ATC	GTT	609
A	I	Q	M	V	L	E	E	K	F	V	Y	K	H	N	V	H	P	L	R	210
GCC	ATC	CAG	ATG	GTG	CTA	GAG	GAG	AAG	TTC	GTC	TAC	AAA	CAC	AAT	GTG	CAC	CCA	CTG	CGG	669
A	V	G	T	E	G	L	F	G	F	V	I	L	S	L	L	L	V	P	M	230
GCA	GTT	GGC	ACT	GAG	GGC	CTC	TTT	GGC	TTT	GTG	ATC	CTC	TCC	CTG	CTG	CTG	GTG	CCC	ATG	729
Y	Y	I	P	A	G	S	F	S	G	N	P	R	G	T	L	E	D	A	L	250
TAC	TAC	ATC	CCC	GCC	GGC	TCC	TTC	AGC	GGA	AAC	CCT	CGT	GGG	ACA	CTG	GAG	GAT	GCA	TTG	789
D	A	F	C	Q	V	G	Q	Q	P	L	I	A	V	A	L	L	G	N	I	270
GAC	GCC	TTC	TGC	CAG	GTG	GGC	CAG	CAG	CCG	CTC	ATT	GCC	GTG	GCA	CTG	CTG	GGC	AAC	ATC	849
S	S	I	A	F	F	N	F	A	G	I	S	V	T	K	E	L	S	A	T	290
AGC	AGC	ATT	GCC	TTC	TTC	AAC	TTC	GCA	GGC	ATC	AGC	GTC	ACC	AAG	GAA	CTG	AGC	GCC	ACC	909
T	R	M	V	L	D	S	L	R	T	V	V	I	W	A	L	S	L	A	L	310
ACC	CGC	ATG	GTG	TTG	GAC	AGC	TTG	CGC	ACC	GTT	GTC	ATC	TGG	GCA	CTG	AGC	CTG	GCA	CTG	969

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Fig. 20B

G W E A F H A L A L Q I L G G F L I L L I G T 330
 GGC TGG GAG GCC TTC CAT GCA CTG CAG ATC CTT GGC TTC CTC ATA CTC CTT ATA GGC ACT 1029

 A L Y N G L H R P L L G G R L S R G R P L 350
 GCC CTC TAC AAT GGG CTA CAC CGT CCG CTG CTG GGC CGC CTG TCC AGG GGC CGG CCC CTG 1089

 A E E S E Q E R L L G G T R T P I N D A 370
 GCA GAG GAG AGC GAG CAG GAG AGA CTG CTG GGT GGC ACC CGC ACT CCC ATC AAT GAT GCC 1149

 S * 372
 AGC TGA 1155

 GGTTCCTGGAGGCTTCTACTGCCACCCGGGTGCTCCTTCTCCCTGAGACTGAGGCCACACAGGCTGGTGGCCCCGAA 1234
 TGCCCTATCCCCAAGGCCTCACCCCTGTCCCCTCCCTGCAGAACCCCGGCGAGCTGCTGCCACAGAAAGATAACAACAC 1313
 CCAAGTCCTCTTTTCTCACTACCACCTGCAGGGTGGTGTACCCAGCCCCCACAAAGCCTGAGTGCAGTGGCAGACCTC 1392
 AGCTCTCTGGACCCCTCCTACAGCAGCTAGAGCTAAATCATGAAGTTGAATTGTAGGAATTTACCACCGTAGTGTATCTG 1471
 AATCATAAACTAGATTATCATATAAAAAAAAAAAAAAAAAAGGGCGGCCGC 1518

Fig. 20C

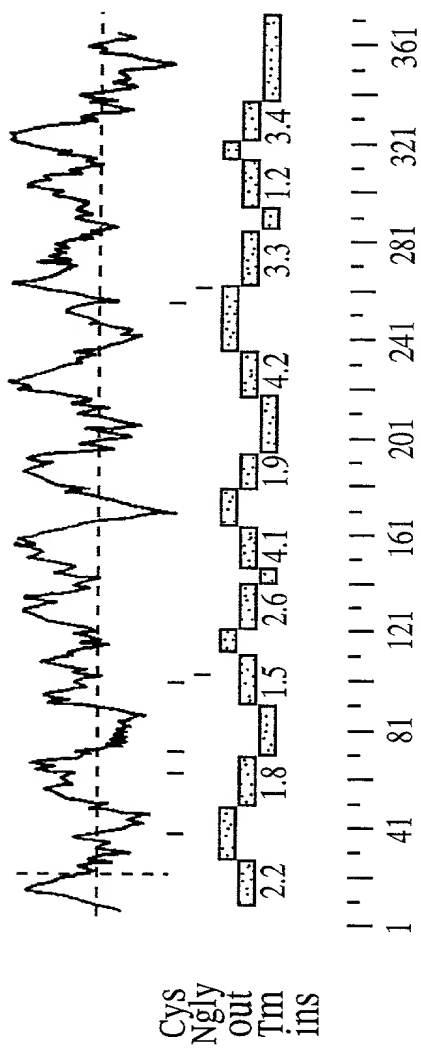


FIG. 20D

GTCGACCCACGCGTCCGGGACAGCTGGCCTGAAGCTCAGAGCCGGGGCTGCGCC																	M	A	P	H	W	5
ATG GCC CCA CAC TGG																						72
A	V	W	L	L	A	A	R	L	W	G	L	G	I	G	A	E	V	W	W	25		
GCT	GTC	TGG	CTG	CTG	GCA	GCA	AGG	CTG	TGG	GGC	CTG	GGC	ATT	GGG	GCT	GAG	GTG	TGG	TGG	132		
N	L	V	P	R	K	T	V	S	S	G	E	L	A	T	V	V	R	R	F	45		
AAC	CTT	GTG	CCG	CGT	AAG	ACA	GTG	TCT	TCT	GGG	GAG	CTG	GCC	ACG	GTA	GTA	CGG	CGG	TTC	192		
S	Q	T	G	I	Q	D	F	L	T	L	T	L	T	E	P	T	G	L	L	65		
TCC	CAG	ACC	GGC	ATC	CAG	GAC	TTC	CTG	ACA	CTG	ACG	CTG	ACG	GAG	CCC	ACT	GGG	CTT	CTG	252		
Y	V	G	A	R	E	A	L	F	A	F	S	M	E	A	L	E	L	Q	G	85		
TAC	GTG	GGC	GCC	CGA	GAG	GCC	CTG	TTT	GCC	TTC	AGC	ATG	GAG	GCC	CTG	GAG	CTG	CAA	GGA	312		
A	I	S	W	E	A	P	V	E	K	K	T	E	C	I	Q	K	G	K	N	105		
GCG	ATC	TCC	TGG	GAG	GCC	CCC	GTG	GAG	AAG	AAG	ACT	GAG	TGT	ATC	CAG	AAA	GGG	AAG	AAC	372		
N	Q	T	E	C	F	N	F	I	R	F	L	Q	P	Y	N	A	S	H	L	125		
AAC	CAG	ACC	GAG	TGC	TTC	AAC	TTC	ATC	CGC	TTC	CTG	CAG	CCC	TAC	AAT	GCC	TCC	CAC	CTG	432		
Y	V	C	G	T	Y	A	F	Q	P	K	C	T	Y	V	V	S	A	A	L	145		
TAC	GTC	TGT	GGC	ACC	TAC	GCC	TTC	CAG	CCC	AAG	TGC	ACC	TAC	GTC	GTG	AGT	GCT	GCC	CTC	492		

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Fig. 21A

L	P	R	C	P	Q	P	P	A	L	L	T	L	L	W	T	R	G	C	G	165
CTA	CCT	CGG	TGT	CCC	CAG	CCC	CCC	GCC	CTC	CTC	ACC	CTT	CTC	TGG	ACT	CGT	GGA	TGT	GGC	552
P	Q	S	P	A	L	K	H	L	L	I	T	S	L	S	V	L	R	T	C	185
CCA	CAG	AGC	CCT	GCC	CTT	AAG	CAT	CTC	ATC	ACC	TCT	CTC	TCT	TCT	GTC	CTT	AGA	ACA	TGC	612
S	P	S	L	W	S	M	E	S	L	K	M	G	R	A	S	V	P	M	T	205
TCA	CCT	TCA	CTT	TGG	AGC	ATG	GAG	AGT	TTG	AAG	ATG	GGA	AGG	GCA	AGT	GTC	CCT	ATG	ACC	672
Q	L	R	A	M	L	A	F	L	W	M	V	S	C	T	R	P	H	S	T	225
CAG	CTA	AGG	GCC	ATG	CTG	GCC	TTC	TTG	TGG	ATG	GTG	AGC	TGT	ACT	CGG	CCA	CAC	TCA	ACA	732
T	S	W	A	R	N	P	L	S	C	V	T	W	G	P	T	T	P	*		244
ACT	TCC	TGG	GCA	CGG	AAC	CCA	TTA	TCC	TGC	GTA	ACA	TGG	GGC	CCC	ACC	ACT	CCA	TGA		789
AGACAGAGTACCTGGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCTATGTACCTGAGAGTGTGGCAGCTT																				868
CACGGGGACGACGACAAGGTCTACTTCTTCTTCAGGGAGCGGGCAGTGGAGTCCGACTGCTATGCCGAGCAGGTGGTG																				947
GCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGGGGGCGCACGGACCCCTGCAGAGGAAGTGGAACACCGTTCTCTGAAGG																				1026
CGCGGCTGGCATGCTCTGCCCCGAACTGGCAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCCTGCAGGACACCTC																				1105

Fig. 21B

CTGGCACAACACCCTTCTTTGGGGTTTTTCAAGCACAGTGGGTGACATGTACCTGTGGCCATCTGTGAGTACCAG 1184
TTGGAAGAGATCCAGCGGGTGTGTGAGGGCCCCCTATAAGGAGTACCATGAGGAAGCCAGAAAGTGGACCGCTACACTG 1263
ACCCGTGTACCCAGGCCCTGGTTGTGATGGCTGCCCAGCCCCGCCCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAG 1342
GGGGCGCGGCTGGCTGCTGAAGGCTACCTTGTGGCTGTCTGTGCAGGCCCGCTCGGTGACCTTGGAGGCCCGGGCCCCC 1421
TGGAAAACCTGGGGCTGGTGTGGCGTGGTGGCCCCCTGGGGGCTGTGTGCCCTGGTGTGCTGTGCTGTGCTGTG 1500
ATTGCGCCGGCGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAGGCTACTGAGAGGACCTTGGTGTACCCCCCTGGAGCTG 1579
CCCAAGGAGCCACCAAGTCCCCCTTCCGGCCCCGTCTCTGAACCAGATGAGAAACTTTGGGATCCTGTGCGGTACTACT 1658
ATTCAGATGGCTCCCTTAAGATAGTACCTGGGCAATGCCCGGTGCCAGCCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGG 1737
CATCCCAGGCCAGCCTCTGCCCTTCTCCAACCTCGGCTTCACCTGGGGGTGGCGGAACTCAAAATGCCAATGGTTACGTG 1816
CGCTTACAAC TAGGAGGGAGGACCGGGAGGGCTCGGGCACCCCCCTGCCCTGAGCTCGCGGATGAACCTGAGACGCAAAC 1895
TGCAGCAACGCCAGCCACTGCCCCGACTCCAACCCCCGAGGAGTCAATCAGTATGAGGGGAACCCCCACCGCTCGGCGGGA 1974
AGCGTGGGAGGTAGCTCCTACTTTTGCACAGGCACCAAGCTACCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGG 2053

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Fig. 21C

GACAGATACTGCCAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCACTTGGTGTGGCTCAC	2132
CAGGGCACAGCCTCGCAGAAGGCATCTTCCTCTCTGTGAATCACAGACACGCGGACCCAGCCGCCAAAACCTTT	2211
TCAAGGCAGAAAGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTATGTGTGTGCACGC	2290
GGGTGCGCGCTTGTGGCATAGCCCTTCCTGTGTTTCTGTCAAAGTCTTCCCTTGGCCTGGGTCCCTCCTGGTGAGTCATTGGAG	2369
CTATGAAGGGGAAGGGTCTGTATCACTTTGTCTCTCTACCCCCCACTGCCCCGAGTGTCTGGGCAGCGATGTACATATGG	2448
AGGTGGGGTGGACAGGGTGTCTGTGCCCCCTTCAGAGGGAGTGCAGGGCTTGGGGTGGGCCCTAGTCCTGCTCCTAGGGCTG	2527
TGAATGTTTTTCAGGGTGGGGGAGGAGATGGAGCCCTCCTGTGTGTTTGGGGGGAAGGGTGGGTGGGGCCTCCCACCTTG	2606
GCCCCGGGGTTCAGTGGTATTTTATACTTGCCCTTCTCTGTACAGGGCTGGGAAAGGCTGTGTGAGGGGAGAGAAGGG	2685
AGAGGGTGGGCCCTGCTGTGGACAAATGGCATACTCTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAACCTTATTGT	2764
GTCCCCGCGTATTATTGTTGTAATAATTTGAGATTTTATATATGA	2811

Fig. 21D

150

Fig. 21F

Cellar

```

710      720      730      740      750      760      770
M ASERTLVYPLELPKEPASPFRPGPETDEKLWDPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQP
H -----W-----GPTTP-----
      :
      :: ::
      240

780      790      800      810      820      830
M LPSPTRLHGGGRNSNANGYVRLQLGGEDRGSGHPLPELADELRRKLQQRQLPDSNPPESSV
H -----

```

Fig. 21H

```

360      370      380      390      400      410      420
M QAQKWARYTDPVSPRPGSCINNWHRDNGYTSSELPLDNTINFIKKHPLMEDQVKPRLGRPLLVKKNNTNF
  ::      ::      ::      ::      ::      ::      ::
H ----WTR-----GCGPQ-----SPAL-----KH-----LLI---TSL
160
430      440      450      460      470      480      490
M THVVADRVPGLDGATYTVLFIGTGDWLLKAVSLGPWIHMVEELQVFDQEPVESLVLSQSKKVLFAGSRS
  .      .      .      .      .      .      .
H S-----VLRTCSPSLW-----SMESLKMGRA-----SVPMT
180
500      510      520      530      540      550      560
M QLVQLSLADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVR
  ::      ::      :      :      :      :      :
H QLRAM-LA-----F-----L-----WMVSCTRPHSTTS-----
210
570      580      590      600      610      620      630
M SIPKNITVVSGTDLVLPCHLSSNLAAHAWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYS
  :
H -----W-----
640      650      660      670      680      690      700
M EEQGTRLAAESYLVAVVAGSSVTLEARAPLENLGLVWLAVVALGAVCLVLLLVLSLRRRLREELEKGA
  ::      ::      ::      ::      ::      ::      ::
H -----ARNPLS-----CVT-----
230

```

Fig. 21G

Figure 21I

```

10      20      30      40      50      60      70
M GGCACGAGTGGCCGGAGTCAAACGCGAGGCGCAGCCAGGGATTGGAGCTGCACGAAAGAGGGCTGCTG
: :      : : : :      : : : :      : : : :      : : : :      : : : :
H GTC-----GACC-----CACG-----CGTC-----CGCG-----GGACAGCTG
10      20

80      90      100     110     120     130     140
M GACTGAAGTTTAGACCCCTGGGTGTCTGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAGGGCT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCCTGAAGCTCAGAGCCGGGGCGTGGCCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCT
30      40      50      60      70      80      90

150     160     170     180     190     200     210
M GTGGGGCCCTGGGCATCGGGGCTGAGATGTGGTGGAACCTTGTGCCCGGAAGACAGATATCTTCTGGGAG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTGGGGCCCTGGGCATTGGGGCTGAGGTGTGGTGGAACCTTGTGCCCGGTAAGACAGTGTCTTCTGGGAG
100     110     120     130     140     150     160

220     230     240     250     260     270     280
M CTGGTCACAGTAGTGAGCGGGTCTCCACAGACAGGCATCCAGGACTTCCTGACACTGACCCCTGACAGAAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTGGCCACGGTAGTACGGCGGTCTCCACAGACCGGCATCCAGGACTTCCTGACACTGACGCTGACGGAGC
170     180     190     200     210     220     230

290     300     310     320     330     340     350
M ATTCTGGCCTTTTATATGTGGGGGCCCCGAGAGGGCGCTGTTTGCCTTCAGTGTAGAGGCTCTGGAGCTGCA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CCACTGGGCTTCTGTACGTGGGGGCCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCCCTGGAGCTGCA
240     250     260     270     280     290     300

```

Fig. 21I

```

360      370      380      390      400      410      420
M AGGAGCGATCTCTTGGGAGGCTCCAGCTGAGAGAAATGAATGTACCCAGAAAGGAGCAACACAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGGAGCGATCTCTTGGGAGGCCCCCGTGGAGAGAAAGACTGAGTGTATCCAGAAAGGAGCAACACAG
310      320      330      340      350      360      370

430      440      450      460      470      480      490
M ACCGAATGCTTCAACTTCATCCGCTTCCTTCAGCCATACAATTCCTCCCATCTGTATGTCTGCGGCACCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACCGAGTGCTTCAACTTCATCCGCTTCCTGCAGCCCCATAAATGCCTCCACCTGTACGTCTGTGGCACCT
380      390      400      410      420      430      440

500      510      520      530      540      550      560
M ATGCCTTCCAGGCCCAAGTGCACCTACATCAACATGCTCACGTTACCTTGGACCGTGCAGAAATTGAGGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACGCCTTCCAGGCCCAAGTGCACCTACGTCG-----TGA---GTGC-----
450      460      470      480      490      500      510

570      580      590      600      610      620      630
M TGGGAAGGGTAAATGCCCATATGACCCAGCTAAGGGTCACACCCGGACTCCTTGTGGACGGTGAGCTGTAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H -----TGCCCT-----CCTACCTCGGTGTC-C-CCAGCCCC-----CG-----C
490      500      510

640      650      660      670      680      690      700
M TCAGCCACACTCAATAACTTCCTGGGCACAGAGCCGGTTATCCTTCGATACATGGGACCCACCACTCCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CCT-CCTCACCC---TTCT--CTGGACTCGTGG-----ATGTGG-CCCAC-----
520      530      540      550

```

Fig. 21J

Sequence Alignment

```

710      720      730      740      750      760      770
M TCAAGACAGTACCTGGCTTTTGGCTGAATGAACCCCACTTTGTAGGCTCTGCCTTTGTCCCTGAGAG
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGAGCCCTGCCCTTAAGC-----ATCTCCTCATCAC---CTCTCTCTGTCC-TTAGA-
560      570      580      590      600

780      790      800      810      820      830      840
M TGTGGGAAGCTTACGGGAGACGATGACAAGATCTACTTCTTTCAGTGAGCGGCAGTGAGATGAC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----ACATGCTCACCTTCA-CTT-TG-GAGCA---TGGAGAGTTTGA-
610      620      630      640

850      860      870      880      890      900      910
M TGCTATTCCGAGCAGGTGGTGGCTCGTGTGGCGAGAGTCTGTAAAGGTGACATGGGGGAGCACGACGC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGATGG-----GAAGGGCAAGTGTG-----C-----CTATGACCC
650      660      670

920      930      940      950      960      970      980
M TGCAGAAAGAAATGGACGACGTTCCCTGAAGGCTCGGTTGGTGTGCTCAGCCCCCTGACTGGAAGTCTACTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H AGCTAAGGGCCATGCTGGCCCTTCTTGT-GGATGTTGAGCTGTACTCGGCCAC--ACT-----CAACAA
680      690      700      710      720      730

990      1000     1010     1020     1030     1040     1050
M CAACCAGCTGAAGGCGGTGCACACCCCTGCGGGGCGCCCTCTTGGCACAAACACCACTTCTTCGGGTTTTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H CTTCCCTG-----GGCA-----CGGAAC-CCA-TTATC-----CTGCG-----TAA
740      750      760

```

Fig. 21K

```

1060      1070      1080      1090      1100      1110      1120
M CAAGCGGATGGGGCGATATGGACCTGTCTGCAGTTTGTGAGTACCAGTTGGAACAGATCCAGCAAGTGT
::      :::::      ::      ::::      :      ::::
H CA-----TGGGGC-----CC--C-----ACCA-----C---TCCA-----
770

1130      1140      1150      1160      1170      1180      1190
M TTGAGGTCCTACAAGGAGTACAGTGAGCAAGCCAGAAAGTGGCCCCGTATACTGACCCGGTACCCAG
::::      ::      :::::      :::::      ..      ::      ::      ::      ::
H -TGAAG-----ACA--GAGTAC-----CTGGCC---TTTGGCTCAACGAACCTCACTTTGTA---GG
790      800      810      820      830

1200      1210      1220      1230      1240      1250      1260
M CCCTCGGCCTGGTTCGTGTATCAACAACACTGGCACCCGAGACAATGGCTACACCAGTTCCTGGAAC TGCCG
:      ::      :::::      :::::      ::::      ::      ::      ::      ::
H C--TCTGCCTA-----TGTA-C-----CTGA-----GAGT-GTGGGCAGCTTCA---CGGGGGACGAC--
840      850      860      870      880

1270      1280      1290      1300      1310      1320      1330
M GACAACACCCCTCAACTTCATCAAGAAGCACCCCTGATGGAGGACCAGGTGAAGCCTCGGTTGGGCCGCC
:::::      .      :      :::::      :::::      ::::      :      :::
H GACAAGGTCTACTTCTTCTCAGGGAGC-----GGGC--AGTGGAGTC-CGA-----
890      900      910      920

1340      1350      1360      1370      1380      1390      1400
M CCCTACTTGTGAAGAAGAACACTAACTTCACACACGTGGTGGCCGACAGGGTCCAGGCTTGATGGTGC
:::::      ::      .      .      .      :::::      ::      ::      ::
H --CTGCTA-----TGC--CGAGCAGGTGGTGGC-----TC-----GTGTGGC
930      940      950

```

Fig. 21L

Sequence alignment

```

1410      1420      1430      1440      1450      1460      1470
M CACCTATACAGTGTGTTTCATTGGTACAGGAGATGGCTGGCTGCTGAAGGCTGTGAGCCTGGGGCCCTGG
:  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
H C--CGTGTCTG-----CAAGGG--C--GATATGGGGGC-----GCA-----C--GGACCCCTG-
960                                     970      980      990

1480      1490      1500      1510      1520      1530      1540
M ATCCACATGGTGGAGGAACTGCAGGTGTTTGACCAGGAGCCAGTGGAAGTCTGTGCTGTCTCAGAGCA
::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
H -----CA-----GAGGAA-----GTG-----GACCACGTTCCCTG-----AAGGC-----GCGG---CTG-GCA
1000                                1010      1020      1030

1550      1560      1570      1580      1590      1600      1610
M AGAAGGTGCTCTTTGCTGGCTCCCGCTCTCAGCTGGTTTCAGCTGTCTCTGCGCGACTGCACAAAGTACCG
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H -----TGCTCT-----GC-CCCGAACT-GGCAG-CTCTACT-TCA---ACCAGCTGCA---GG---CG
1040                                1050      1060      1070      1080

1620      1630      1640      1650      1660      1670      1680
M TTTCTGTAGACTGTGTCCTGGCCAGGGACCCCTTACTGTGCTGCTGGAATGTCAACACCAGCCGCTGTGTG
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H ATGC-----ACA---CCCTG--CAGGACACCT-----CCTGGCA---CAACACCACCTTCTTTGGG
1090                                1100      1110      1120      1130

1690      1700      1710      1720      1730      1740      1750
M GCCACCACCAAGTGTGCTCGGCTCGGGGTCCCTTTCTGTGTCCAACATGTGGCGAACTTGGACACTTCAAAGATGT
:  .  .  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H GTTT--TTCAA-----GCACAGTGG-----GGT--GACATGTACCTGTC---GGC-CATCTG---TGA
1140                                1150      1160      1170

```

Fig. 21M

```

1760      1770      1780      1790      1800      1810      1820
M GTAACCAGTATGGCATTAATAAAGTCAGATCTATTCCCAAGAACAATCACCGTTGTGTCAGGCACAGACCT
  :: ::::: ::::      ::::      ::::      ::::      ::::      ::::
H GTA-CCAGT-TGG-----AAG--AGATC-----CAGCG--GGTGTTTGAGG-----
1180      1190      1200      1210

1830      1840      1850      1860      1870      1880      1890
M GGTCCTACCCCTGCCACCTCTCGTCCAATTGGCCCATGCCCACTGGACCTTCGGAAGCCAGGACCTGCCT
  ::::      ::::: ::::: :::::      ::::      ::::      ::::: ::::
H -----GCC-----CCTATAAGGA--GTACC---ATGA-----GGAAGC-----CCA
1220      1230      1240

1900      1910      1920      1930      1940      1950      1960
M GCAGAAACAACCTGGCTCCTTTCTTTATGACACGGGACTCCAGGCGCTGGTGTGATGGCCGCACAGTCCC
  : :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::
H GAAGTGGGACC--GCTAC--ACT---GACCCCTGTAC-CCAGGCCCTGGTTGTGATGGCTGCCCAAGCCCC
1250      1260      1270      1280      1290      1300

1970      1980      1990      2000      2010      2020      2030
M GTCACCTCTGGACCCCTATCGTTGCTATTTCAGAGGAGCAGGGACAAGACTGGCTGCAGAAAGCTACCTTGT
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAGGGGCGCGGCTGGCTGCTGAAGGCTACCTTGT
1310      1320      1330      1340      1350      1360      1370

2040      2050      2060      2070      2080      2090      2100
M TGCTGTCTGTCGGCCGGCTCGTCCGTGACACTGGAGGCACGGGCTCCCTTGAAAAACCTGGGGCTCGTGTGG
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H GGCTGTCTGGCAGGCCCGTCGGTGACCTTGGAGGCCCGGGCCCCCTGAAAAACCTGGGGCTGGTGTGG
1380      1390      1400      1410      1420      1430      1440

```

Fig. 21N

```

2110      2120      2130      2140      2150      2160      2170
M CTCGCTGTGTGGCCCTGGGGGCTGTGTGCCTGGTGTCTGTCTATCGTCCGCCGGCGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTGGCGGTGTGGCCCTGGGGGCTGTGTGCCTGGTGTCTGTCTGTCTATTCGCCCGGGCGGC
1450      1460      1470      1480      1490      1500      1510

2180      2190      2200      2210      2220      2230      2240
M TTCGAGAAGAGCTAGAAAAGGTGCCAAGCATCTGAGAGGACACTGGTGATCCCTTGGAAC TGCCCAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TCGGGGAAGAGCTGGAGAAAAGGGCCCAAGCTACTGAGAGGACCTTGGTGATCCCTTGAGCTGCCCAA
1520      1530      1540      1550      1560      1570      1580

2250      2260      2270      2280      2290      2300      2310
M GGAGCCTGCCAGTCCCCCCTTCCCGTCTCCGCCCGAAACTGATGAGAAACTTTGGGATCCTGTGCGGTAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GGAGCCCACCAAGTCCCCCCTTCCGGCCCTGTCTGAACCAAGATGAGAAACTTTGGGATCCTGTGCGGTAC
1590      1600      1610      1620      1630      1640      1650

2320      2330      2340      2350      2360      2370      2380
M TACTATTCGGATGGCTCTCTCAAGATTGTGCTGCACGCCCCGGTGCCAGCCTGGGGGTGGGCCCCCCTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TACTATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCCCGGTGCCAGCCCGGTGGGGGCCCCCCTT
1660      1670      1680      1690      1700      1710      1720

2390      2400      2410      2420      2430      2440      2450
M CCCCACCTCCTGGCATACCTGGCCAGCCTCTGCCTTCTCCAACCTCGGCTCCACCTAGGAGTGTGCGGAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CGCCACCTCCAGGCATCCCAGGCCAGCCTCTGCCTTCTCCAACCTCGGCTTCACCTGGGGGTGGGCGGAA
1730      1740      1750      1760      1770      1780      1790

```

Fig. 210

[illegible]

Fig. 21P

```

2800      2810      2820      2830      2840      2850      2860
M ACTTCAGCCCTCACAGGAGACA-CACCCCTCCTCT--GTGAATTTGAGACATGTGGGACCCAGCAGCCAAA
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCACCAAGCCTCGCAGAAGGCATCTTCCTCCTCTCTGTGAATCACAGACACGCGGACCCAGCCGCCCCAAA
2140      2150      2160      2170      2180      2190      2200

2870      2880      2890      2900      2910      2920
M ACTTTGCAAGGAAGAGGTTTCAAGATGTGGCGTGTTGTGCAT--ATATGTTGGTATGCATGTGGAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACTTTTCAAGGCAGAAAGTTTCAAGATGTGTGTTGTCTGTATTTGCACATGTGTTGTGTGTGTGTAT
2210      2220      2230      2240      2250      2260      2270

2930      2940      2950      2960      2970      2980      2990
M GAATGTGTGTGTGTGTG---TGTTGTGTAACTTTCCTGTCTCTATCACGCTTTCCTTGGCCTGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTGTGTGTGCACGCGCGTGTGCGCCTTGTGGCATAAGCCTTCCTGTTTCTGTCAAGTCTTCCCTTGGCCTGG
2280      2290      2300      2310      2320      2330      2340

3000      3010      3020      3030      3040      3050      3060
M GGTCCCTCCTGTTGAGTCTTTGGAGCTATGAAGGGGAAGGGGTCATAGCACATTTGCTTCTCCTACCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H G-TCCTCCTGGT-GAGTCATTGGAGCTATGAAGGGGAAGGGG-TCGTATCACATTTGTCTCTCCTACCCCC
2350      2360      2370      2380      2390      2400      2410

3070      3080      3090      3100      3110      3120      3130
M AGCTGTCCCAAGCTTTGGGGCAGTGATGTACATACGGGGAAGGAAGGACAGGGTGTGTACCCCTTTTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H A-CTGCCCCCGAG-TGTCGGGCAGCGATGTACATATGGAGGTGGGGTGGACAGGGTGTGTGCCCTTTCAG
2420      2430      2440      2450      2460      2470      2480

```

Fig. 21Q

```

3140      3150      3160      3170      3180      3190      3200
M GGGAGTGCAGGCTCGGGGTGGCCCTAGCCCTGCTCCTAGGGCTGTGAATGTTTCAGGGCGGGGTT
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGGAGTGCAGGCT-TGGGGTGGCCCTAGTCTGCTCCTAGGGCTGTGAATGTTTCAGGGTGGGGGA
2490      2500      2510      2520      2530      2540      2550

3210      3220      3230      3240      3250      3260      3270
M GGGGTGGAGATGGAACCTCCTGC--TTCAGGGGAGGGTGGCAGGGCCTCCCACTTGCCCTCCGGG
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H GGG-----AGATGGAGCCTCCTGTGTGTTTGGGGGAAGGTGGTGGGCCTCCCACTTGCCCCCGGGG
2560      2570      2580      2590      2600      2610

3280      3290      3300      3310      3320      3330
M TTCGGTGGTATTTATATTTCGGCTCTTC-TG-ACAGGCTGGGAAGG--TTGTGGGGGAGGAAGG
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H TTCAGTGGTATTTATACCTTGCCCTTCTTCCTGTACAGGCTGGGAAAGCTGTGTGAGGGGAGAGAAAGG
2620      2630      2640      2650      2660      2670      2680

3340      3350      3360      3370      3380      3390      3400
M AGGAGTGGGCATGCTATGGATACTGGCCCTATCCTCCTGCTCTGGGAAAAGGCT---AACAGTGA
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGAGGTGGCCCTGCTGTGGACAAATGCATACCTCTCTCCAGCCCTAGGAGGAGGCTCCTAACAGTGA
2690      2700      2710      2720      2730      2740      2750

3410      3420      3430      3440      3450      3460      3470
M ACTTATTGTGTCCCCACATATTTATTGTTGTAAATATTTGAGTATTTTATATTGACAAATAAATGGA
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H ACTTATTGTGTCCCCGCTATTTATTGTTGTAAATATTTGAG-ATTTTATATTGA-----
2760      2770      2780      2790      2800      2810

```

Fig. 21R

GTCGACCCACGCGTCCGCGGACGCGTGGGCGCGCGGGGCCATCCAGACCCCTGCGGAGAGCGAGGCCCGAGCGTCGCC 79
 GAGGTTTGAGGCGCGGAGACCGAGGGCCTGGCGGCCGAAGAACCGCCCCCAAGAGAGCCCTCTGGCCCCGGGGGCTGC 158
 TGGAACATGTGCGGGGGACACAGTTTGTGACAGTTGCCAGACT ATG TTT ACG CTT CTG GTT CTA CTC 8
 228
 S Q L P T V T L G F P H C A R G P K A S 28
 AGC CAA CTG CCC ACA GTT ACC CTG GGG TTT CCT CAT TGC GCA AGA GGT CCA AAG GCT TCT 288
 K H A G E E V F T S K E E A N F F I H R 48
 AAG CAT GCG GGA GAA GAA GTG TTT ACA TCA AAA GAA GAA GCA AAC TTT TTC ATA CAT AGA 348
 R L L Y N R F D L E L F T P G N L E R E 68
 CGC CTT CTG TAT AAT AGA TTT GAT CTG GAG CTC TTC ACT CCC GGC AAC CTA GAA AGA GAG 408
 C N E E L C N Y E E A R E I F V D E D K 88
 TGC AAT GAA GAA CTT TGC AAT TAT GAG GAA GCC AGA GAG AGT TTT GTG GAT GAA GAT AAA 468
 T I A F W Q E Y S A K G P T T K S D G N 108
 ACG ATT GCA TTT TGG CAG GAA TAT TCA GCT AAA GGA CCA ACC ACA AAA TCA GAT GGC AAC 528

Fig. 22A

R E K I D V M G L L T G L I A A G V F L 128
 AGA GAG AAA ATA GAT GTT ATG GGC CTT CTG ACT GGA TTA ATT GCT GCT GGA GTA TTT TTG 588

 V I F G L L G Y Y L C I T K C N R L Q H 148
 GTT ATT TTT GGA TTA CTT GGC TAC TAT CTT TGT ATC ACT AAG TGT AAT AGG CTA CAA CAT 648

 P C S S A V Y E R G R H T P S I I F R R 168
 CCA TGC TCT TCA GCC GTC TAT GAA AGG GGG AGG CAC ACT CCC TCC ATC ATT TTC AGA AGA 708

 P E A A L S P L P P S V E D A G L P S 188
 CCT GAG GAG GCT GCC TTG TCT CCA TTG CCG CCT TCT GTG GAG GAT GCA GGA TTA CCT TCT 768

 Y E Q A V A L T R K H S V S P P P Y P 208
 TAT GAA CAG GCA GTG GCG CTG ACC AGA AAA CAC CAC AGT GTT TCA CCA CCA CCA CCA TAT CCT 828

 G H T K G F R V F K K S M S L P S H * 227
 GGG CAC ACA AAA GGA TTT AGG GTA TTT AAA AAA TCT ATG TCT CTC CCA TCT CAC TGA 885

 CTACCTTGTCATTTGGTATAAGAAATTTGTGTATTGTATAGCCGGCATGGTGGCTCATGCGCTGTAATCCAGCAC 964

 TTTGGAGGCCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACCCGGTCTCTACTAAAAATTCAAAAATTACCTA 1043

 GCGGTCAATGGGGCATGCCCTGTAGTCCCACCTACTTGGAGGCTGAAGCAGGAGAAATTGCTCGAACCTGGGAGGCAGAGG 1122

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Fig. 22B

[illegible]

Fig. 22C

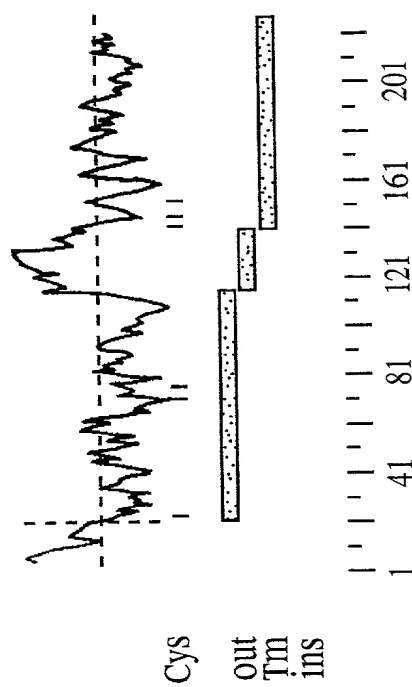


FIG. 22D

GTCGACCCAC	GGTCCGCTG	CGTCTCACC	CCTGGACCAC	CCTGGGAGAA	CAGTTGACCG	60
AAGTTTGTTT	GGCAGTTGCT	GCTGGACT	ATG TTT CTG	CTT CTG	GTA CTC	112
	Met	Phe	Leu	Leu	Val	Leu
	1					5
AGC CAG CTG	CCC AGA CTT	ACC CTC	GCG GTT	CCT CAT	ACA AGA AGC CTA	160
Ser Gln	Leu Pro	Arg Thr	Leu Ala	Val Pro	His Thr	Arg Ser
	10					20
AAG AAT TCT	GAA CAT GCC	CCA GAA	GGA GTC	TTT GCA	TCA AAA AAA GCA	208
Lys Asn	Ser Glu	His Ala	Pro Glu	Gly Val	Phe Ala	Ser Lys
	25					40
						35
GCA AGC ATC	TTT ATG CAC	CGT CGC	CTC CTA	TAC AAT	AGA TTT GAT TTA	256
Ala Ser	Ile Phe	Met His	Arg Arg	Leu Tyr	Asn Arg	Phe Asp
		45				55
GAA CTC TTC	ACT CCC	GGG AAC	CTG GAG	AGA GAG	TGC TAT	GAG GAG
Glu Leu	Phe Thr	Pro Pro	Gly Asn	Leu Leu	Glu Arg	Glu Glu
	60					70
						65
TGT AGT TAT	GAA GAA	GCC AGA	GAG ATC	CTC GGG	GAC AAC	GAA GAA
Cys Ser	Tyr Glu	Glu Glu	Ala Arg	Glu Ile	Leu Gly	Asn Glu
	75					85
						80

Fig. 22E

ATC ACA TTC TGG CGG GAA TAT TCA GTC AAA GGA CCA ACC ACA AGA TCA	400
Ile Thr Phe Trp Arg Glu Tyr Ser Val Lys Gly Pro Thr Thr Arg Ser	
90	
GAT GTC AAC AAA GAG AAA ATT GAT GTT ATG GGC CTT CTG ACT GGC TTA	448
Asp Val Asn Lys Glu Lys Ile Asp Val Met Gly Leu Thr Gly Leu	
105	
110	
115	
120	
ATT GCG GCT GGA GTA TTC TTG GTT GTT TTT GGC TTA CTT GGT TAC TAT	496
Ile Ala Ala Gly Val Phe Leu Val Val Phe Gly Leu Gly Tyr Tyr	
125	
130	
135	
CTG TGT ATC ACC AAG TGT AAT AGG CAG CCA TAT CAA GGT TCT TCA GCT	544
Leu Cys Ile Thr Lys Cys Asn Arg Gln Pro Tyr Gln Gly Ser Ser Ala	
140	
145	
150	
GTC TAC ACA AGA AGG ACC AGG CAC ACA CCG TCC ATC ATT TTC AGA ACC	592
Val Tyr Thr Arg Arg Thr Arg His Thr Pro Ser Ile Ile Phe Arg Thr	
155	
160	
165	
CAT GAG GAA GCT GTC TTG TCT CCA TCG TCA TCC TCA GAG GAC GCG GGA	640
His Glu Glu Ala Val Leu Ser Pro Ser Ser Ser Ser Glu Asp Ala Gly	
170	
175	
180	

Fig. 22F

CTA CCT TCC TAT GAA CAG GCA GTA GCT CTG ACC AGA AAA CAC AGT GTC	688
Leu Pro Ser Tyr Glu Gln Ala Val Ala Leu Thr Arg Lys His Ser Val	200
185	190
TCA CCA CCA CCT CCA TAT CCT GGG CCA GCA AAA GGA TTT AGG GTA TTT	736
Ser Pro Pro Pro Tyr Pro Gly Pro Ala Lys Gly Phe Arg Val Phe	215
205	210
AAA AAG TCA ATG TCA CTC CCA TCT CAC TAAGCCCAACC TTGCCGCCTT	783
Lys Lys Ser Met Ser Leu Pro Ser His	
220	225
GCTGTGGTCT GAATAATATG TTCCTCCTGA AACAACAACA ACAAAAAAAT TTGCCTGTTC	843
AGCTTTTAT GACAAAGCAC AAGGAATAAA GGAACACTAT ATACAGAACA GAATTCACCA	903
CAGCCCCGCT TTCAGCTCTG CCCCCAAGTG GATTGCTGTC TTGGTAAGAG ACTTCTACCG	963
TGCTTCCTCG AAGTTAAGAA GAAAGTGCCT TTTTGCAATG TAAACTGTAC TGGTTCAAAC	1023
ATTCTTGCTA CAGCTAGGTA CCTATAATCC CCACCTTCAG GAGACTTAGG CGGGAGGGAT	1083
GAGAGTTCAA GGCCAGCCTG GGCCCTGTCA GGACGCTGTC TCAAAACAAA GTTTGTTATC	1143
AATAGAATAA TTAGAATTAA CAAACTAGGA TTTTCAGTCT TAAGTCATGA TATTGGATCT	1203
TCTCTTCAGT AAGGTTTCTT TTTGGCTAGA AATACTTCAT AGAATTTGAC ATTTTGGTAT	1263
ACATCTGTGG CCTTGATACA ATGACTTGAT TTTCTGTTT AATTAGTGCA GAGGATTCAG	1323
CAAATTGCA GGTCTTCATT TTGTTCCCTC GCTATCCATC GATCATGTTT CAGTGTATTA	1383
AGAGGAGTCA GCCAGGCGTG GTGGCCACAC CCTGTGATCC CAGCACTTAG GGGGCATAG	1443
GCAGGCAGAT CTCTGTGAGC TGAAGGACAG CCTGGCCTAC AAAGTCCAGG ACAACCCAGA	1503
CCACACAGAG AAACCTTGTC TTGAAAAACA AAACAACAAAC AAGAGAGAGA GAGAGAGAGA	1563

Fig. 22G

```

GAGAAAAAGAG ATGTCAAGAG GTTTTGT TT TTTT TTTT AAATTACTAT TTATGGGCCT 1623
CACTTGGAAA AGTGCTTGCC ATGCAAAATAG AAGGACAGGA GTTCAATCCT CATTACCCAC 1683
ATTTGAAACA AATAACAAGA AAAACAAAACC AAAAACC CAA AACAACAAA ATCTTGAGAA 1743
CTTGAGTGAA TACCGGTAA CTCAGGGCTA GGCACGTGTA CTGAATCAGG AGCCTCCAGA 1803
TCCAGGGAAA CGCTGTCTCA ACAAATAAAT AAATAAGTAA GTCAGTGAGG TGGTCTTTAA 1863
ACCCAGCACT TGAGAGCCAA AGCAGGCAG AGTCAGTGA GTTGGAGACC AGCCTGGTCT 1923
ACAAAGCAAG TTCTAAGGA GCCAGGCAC AGAGAAACCC TGTCTGAAGG AAAAAAAA 1983
AAAAAAAAG GCGGCGCGC 2002

```

Fig. 22H

```
G      1  ATGTTTCTGCTTCTGGTGGTACTCAGCCAGCTGCCCAGACTTACCCTCGC  50
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
H      1  ATGTTTACGCTTCTGGTCTACTCAGCCAACTGCCACACAGTTACCCTGGG  50

G     51  GGTTCCTCAT...ACAAGAAGCCCTAAAGAATTCTGAACATGCCCCCAGAAG  97
      |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
H     51  GTTCCCTCATTGGCAAGAGAGGTCCAAAGGCTTCTAAGCATGCGGGAGAAG  100

G     98  GAGTCCTTGCATCAAAAAAGCAGCAAGCATCTTTATGCACCGTCGCCCTC  147
      |||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||
H    101  AAGTGTTTACATCAAAAGAAGAAGCAAACTTTTTCATACATAGACGCCCTT  150

G    148  CTATACAAATAGATTTGATTTAGAACTCTTCACCTCCCGGGAACCTGGAGAG  197
      ||  ||  |||||  |||||  ||  |||||  |||||  |||||  |||||  ||  ||
H    151  CTGTATAATAGATTTGATCTGGAGCTCTTCACCTCCCGGCAACCTAGAAAAG  200

G    198  AGAGTGCTATGAGGAGTTCTGTAGTTATGAAGAAAGCCAGAGAGATCCTCG  247
      |||||  |||||  ||  ||  |||||  |||||  |||||  |||||  |||||  ||  ||
H    201  AGAGTGCAATGAAGAACTTTGCAATTATGAGGAAGCCAGAGAGATTTTGTG  250
```

Fig. 22I

G	248	GGGACAAACGAAAGAAATGATCACATTCTGGCGGGAATATT	CAGTCAAAGGA	297
H	251	TGGATGAAGATAAAACGATTGCATTTTGGCAGGAATATT	CAGCTAAAGGA	300
G	298	CCAACCACAAGATCAGATGTCAACAAGAGAAAAT	TGATGTTATGGGCCT	347
H	301	CCAACCACAAAATCAGATGGCAACACAGAGAAAAT	AGATGTTATGGGCCT	350
G	348	TCTGACTGGCTTAATTGCGGCTGGAGTATCTTGGTTGTTT	TGGCTTAC	397
H	351	TCTGACTGGATTAAATTGCTGCTGGAGTATTTTGGTTATT	TGGATTAC	400
G	398	TTGGTTACTATCTGTGTATCACCAAGTGTAATAGGCAGCC	CATATCAAGGT	447
H	401	TTGGCTACTATCTTTGTATCACTAAGTGTAATAGGCTACA	ACATCCATGC	450
G	448	TC TTCAGCTGTCTACACAAGAAAGGACCAGGCACACAC	CCGTC CATTTTT	497
H	451	TC TTCAGCCGTC TATGAAAGGGG...AGGCACACTCCC	TCCATCATTTTT	497

Fig. 22J

```

G      498 CAGAACCCATGAGGAAGCTGTCTTGTCTCCAT...CGTCATCCTCAGAGG 544
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      498 CAGAAACCTGAGGAGGCTGCCCTTGTCTCCATTGCCGCCCTTCTGTGGAGG 547

G      545 ACGCGGGACTACCTTCCTATGAACAGGCAGTAGCTCTGACCAGAAACAC 594
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      548 ATGCAGGATTACCTTCTTATGAACAGGCAGTGGCGCTGACCAGAAACAC 597

G      595 AGTGTCTCACCCACCACCTCCATATCCTGGCCAGCAAAAGGATTTAGGGT 644
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      598 AGTGTTTCACCACCACCACCACCATATCCTGGGCACACAAAAGGATTTAGGGT 647

G      645 ATTTAAAAAGTCAATGTCACCTCCCATCTCAC 675
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      648 ATTTAAAAAATCTATGTCTCTCCCATCTCAC 678

```

Fig. 22K

G 1 MFLLLVLSQLPRLTLAVPH.TRSLKNSEHAPEGVFASKKAASIFMHRRL 49
 H 1 MFLLLVLSQLPRLTLAVPH.TRSLKNSEHAPEGVFASKKAASIFMHRRL 50
 G 50 LYNRFDELFTPGNLERECYEEFCSEYEEAREILGDNEEMITFWREYSVKG 99
 H 51 LYNRFDELFTPGNLERECNEELCNYYEEAREIFVDEDKTIAFWQEYSAG 100
 G 100 PTTTSDVNKEKIDVMGLLTGLIAAGVFLVFGLLGYLYLCITKCNRPYQG 149
 H 101 PTTKSDGNREKIDVMGLLTGLIAAGVFLVIFGLLGYLYLCITKCNRLQHP 150
 G 150 SSAVYTRRRTRHTPSIIFRTHHEEAVLSP.SSSSEDAGLPSYEQAVALTRKH 198
 H 151 SSAVY.ERGRHTPSIIFRRPEEAALSPPLPPSVEDAGLPSYEQAVALTRKH 199
 G 199 SVSPPPPPYPAKGFVFKKMSMLPSH 225
 H 200 SVSPPPPPYPGHTKGFRVFKKMSMLPSH 226

Fig. 22L

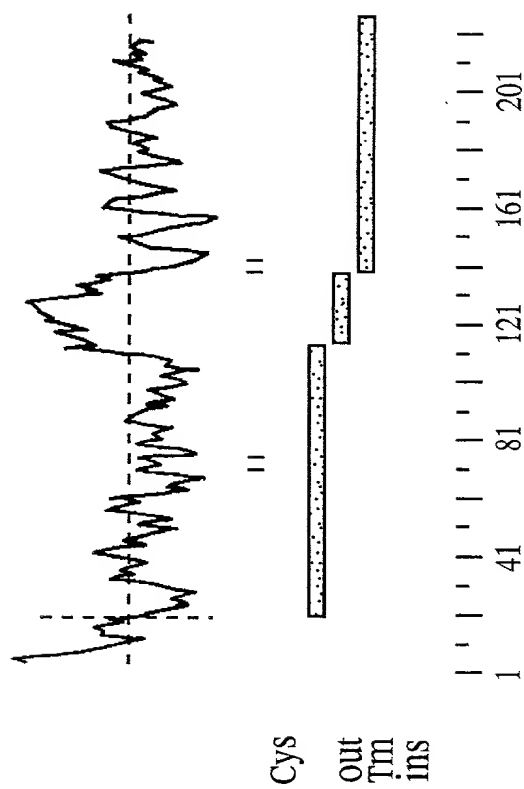


FIG. 22M

Sequence

T	Y	G	P	D	C	L	A	C	Q	G	G	S	Q	R	P	C	S	G	N	151
ACC	TAC	GGT	CCC	GAC	TGT	CTC	GCA	TGC	CAG	GGC	GGA	TCC	CAG	AGG	CCC	TGC	AGC	GGG	AAT	566
G	H	C	S	G	D	G	S	R	Q	G	D	G	S	C	R	C	H	M	G	171
GGC	CAC	TGC	AGC	GGA	GAT	GGG	AGC	AGA	CAG	GGC	GAC	GGG	TCC	TGC	CGG	TGC	CAC	ATG	GGG	626
Y	Q	G	P	L	C	T	D	C	M	D	G	Y	F	S	S	L	R	N	E	191
TAC	CAG	GGC	CCG	CTG	TGC	ACT	GAC	TGC	ATG	GAC	GGC	TAC	TTC	AGC	TCG	CTC	CGG	AAC	GAG	686
T	H	S	I	C	T	A	C	D	E	S	C	K	T	C	S	G	L	T	N	211
ACC	CAC	AGC	ATC	TGC	ACA	GCC	TGT	GAC	GAG	TCC	TGC	AAG	ACG	TGC	TCG	GGC	CTG	ACC	AAC	746
R	D	C	G	E	C	E	V	G	W	V	L	D	E	G	A	C	V	D	V	231
AGA	GAC	TGC	GGC	GAG	TGT	GAA	GTG	GGC	TGG	GTG	CTG	GAC	GAG	GGC	GCC	TGT	GTG	GAT	GTG	806
D	E	C	A	A	E	P	P	P	C	S	A	A	Q	F	C	K	N	A	N	251
GAC	GAG	TGT	GCG	GCC	GAG	CCG	CCT	CCC	TGC	AGC	GCT	GCG	CAG	TTC	TGT	AAG	AAC	GCC	AAC	866
G	S	Y	T	C	E	E	C	D	S	S	C	V	G	C	T	G	E	G	P	271
GGC	TCC	TAC	ACG	TGC	GAA	GAG	TGT	GAC	TCC	AGC	TGT	GTG	GGC	TGC	ACA	GGG	GAA	GGC	CCA	926
G	N	C	K	E	C	I	S	G	Y	A	R	E	H	G	Q	C	A	D	V	291
GGA	AAC	TGT	AAA	GAG	TGT	ATC	TCT	GGC	TAC	GCG	AGG	GAG	CAC	GGA	CAG	TGT	GCA	GAT	GTG	986

Fig. 23B

D E C S L A E K T C V R K N E N C Y N T 311
GAC GAG TGC TCA CTA GCA GAA AAA ACC TGT GTG AGG AAA AAC GAA AAC TGC TAC AAT ACT 1046

P G S Y V C V C P D G G G C F E E T E D A C V 331
CCA GGG AGC TAC GTC TGT GTG TGT CCT GAC GGC TTC GAA GAA ACG GAA GAT GCC TGT GTG 1106

P P A E A E A T E G E S P T Q L P S R E 351
CCG CCG GCA GAG GCT GAA GCC ACA GAA GAA AGC CCG ACA CAG CTG CCC TCC CGC GAA 1166

D L * 354
GAC CTG TAA 1175

TGTGCCGGACTTACCCCTTTAAATTATTCAGAAGGATGTCCCGTGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGT 1254

GGACAGCGGGGGAGAGGCTGCCCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGTGTG 243/361 1333

TTCTTAAACAGACTTGTATATTTTGATACAGTTCCTTTGTAATAAAATTGACCATTTGTAGTAATCAAAAAAAAAAAAA 1412

AAAAAGGGCGCGCGCTAGAC 1432

Fig. 23C

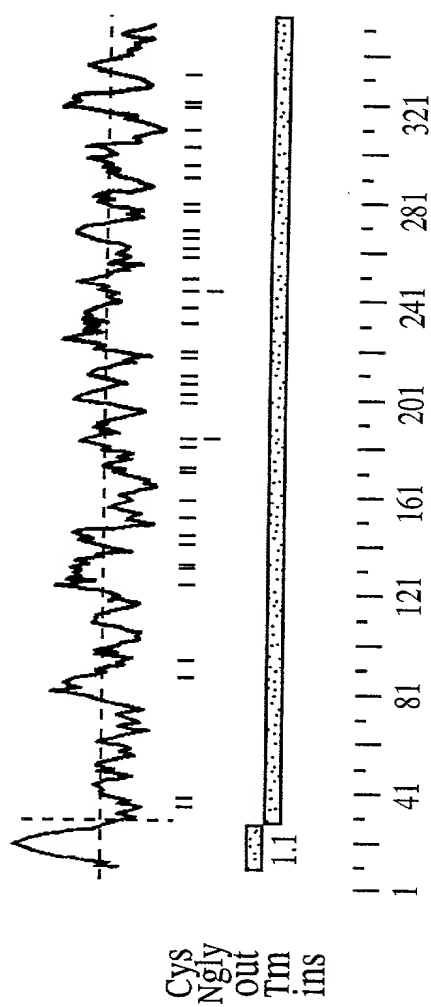


FIG. 23D

Fig. 23F

```

260      270      280      290      300      310      320
C  GGCAACACGGCGTGGAGGAGAAGAGTCTGTCCAAGTACGAATTCAGTGAGATTCGGCTCCTGGAGATTA
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  GGGAACACGGCTTGGAGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCCTGCTGGAGATCC
280      290      300      310      320      330      340

330      340      350      360      370      380      390
C  TGGAGGGCCTGTGTGACAGCAACGACTTTGAATGCAACCAACT-CTTGGAACAGCATGAGGAGCAGCTAG
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  TGGAGGGCCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGC-GCAGGAGGAGCACCTGG
350      360      370      380      390      400      410

400      410      420      430      440      450      460
C  AGGCCTGGTGGCAGACACTGAAGAAGGAGTGCCCTAACCTATTGAGTGGTTCGTGTACACACACTGAA
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  AGGCCTGGTGGCTGCAGCTGAAGAGCGGAATATCCTGACTTATTCGAGTGGTTTGTGTGAAGACACTGAA
420      430      440      450      460      470      480

470      480      490      500      510      520      530
C  AGCATGCTGTCTTCCAGGCACCTATGGGCCAGACTGTGAGGAATGCCAGGTGGGTCTCAGAGGCCCTGT
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  AGTGTGCTGTCTCCAGGAACCTACGGTCCCAGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGC
490      500      510      520      530      540      550

```

Fig. 23G

Fig. 23H

```

      820      830      840      850      860      870      880
C  GCAATGTACAGTACTGTGAAAAATGTCAACGGCTCCTACACATGTGAAGAGTGTGATTCTACCTGTGTGGG
   :: :: ::::::::::::::: : :::::::::::::::::::: : ::::::::::::::: : :::::::::::::::
H  GCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTCGGAAGAGTGTGACTCCAGCTGTGTGGG
   840      850      860      870      880      890      900

      890      900      910      920      930      940      950
C  CTGCACAGGAAAAGGCCAGCCAATTGTAAAGAGTGTATCTCTGGCTACAGCAAGCAGAAAAGGAGAGTGT
   :::::::::::::::::::: : :::::::::::::::::::: : ::::::::::::::: : :::::::::::::::
H  CTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGAGCACGGACAGTGT
   910      920      930      940      950      960      970

      960      970      980      990      1000      1010      1020
C  GCAGATATAGATGAATGCTCATTAGAAACAAGGTGTGTAAGAAAGGAAAATGAGAACTGCTACAATACTC
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : :::::::::::::::
H  GCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTC
   980      990      1000      1010      1020      1030      1040

      1030      1040      1050      1060      1070      1080      1090
C  CAGGAGCTTTGTCTGCGTGTGTCCGGAAGGTTTCGAGGAAGACAGAAAGATGCTTGTGTACAGACAGCAG
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : :::::::::::::::
H  CAGGAGCTACGTCTGTGTGTCTGACGGCTTCGAAGAA-ACGGAAGATGCCTGTGTGCCGCCCGGCAG
   1050      1060      1070      1080      1090      1100      1110

```

Fig. 23I

```

1100      1110      1120      1130      1140      1150
C AAGCGAAGTGCAGAGGAAAGT--CCC-ACACAGCCACCCCTCCCATGAGGATTGTGACGGGCATCCAG
:: :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H AGGCTGAAGCCACAGAGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGA-----CCTG
1120      1130      1140      1150      1160      1170
1160      1170      1180      1190      1200      1210      1220
C GTTCAGAAGCTGGACTCTCACCCCTTTAAAGTTATTGAGAGGACATCCTATAGAAAATGTGCCCCATGGAC
: : :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H --TAATGTGCCGGACTT--ACCCCTTAAATTATTACAGAAAGGATGTCCCGTGGAATAATGTGCCCCTGAGGA
1180      1190      1200      1210      1220      1230

1230      1240      1250      1260      1270      1280      1290
C ATCAACCCCATTTCTCCAGGAAGTTTGG-AGGAAGAAGCTGCCCTGCTTTGAAACAGTAGATACACTCATT
. . : : :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H TGCCGCTCTC----CTGCAGTGGACAGCGGCGGAGAGGCTGCCCTGCTCTCTAACGGTTGATTCTCATTT
1240      1250      1260      1270      1280      1290      1300
1300      1310      1320      1330      1340      1350      1360
C GGCCCTTTAAACGCTGCATTTCTTGTTGGTTCTTTAAACAGATTTCGTATATTTTGATACTGTTCTTTATA
: ::::: : ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H GTCCCTTAAACA-GCTGCATTTCTTGTTGTTCTTTAAACAGACTTGTATATTTTGATACAGTCTTTGTA
1310      1320      1330      1340      1350      1360      1370

1370      1380      1390
C ATAAAAATTGATCATTTGAAGGTCACCAGGAA-----CA-----
: ::::: ::::: ::::: : :::::
H ATAAAAATTGACCATTTGTAGGTAATCAAAAAAATAAAAAAAGGCGCGCGCTAGAC
1380      1390      1400      1410      1420      1430

```

Fig. 23J

GTCGACCCACGCGTCCGTCTGCGGGCCCCAGCCCTCTCCTCAGCTCGCGCAGTCTCCGCCGCGAGTCTCAGCTGCAGCTG 79
CAGGACTGAGCCCGTGACCCCGGAGGAGACCCCGGAGGAGCGACAAACTTCGCAGTGCCCGGACCCCAACCCAGCCCT 158
GGTAGCCTGCAGC ATG GCC CAG CTG TTC CTG CCC CTG CTG GCA GCC CTG GTC CTG GCC CAG 16
220
A P A A L A D V L E G D S S E D R A F R 36
GCT CCT GCA GCT TTA GCA GAT GTT CTG GAA GGA GAC AGC TCA GAG GAC CGC GCT TTT CGC 280
V R I A G D A P L Q G V L G G A L T I P 56
GTG CGC ATC GCG GGC GAC GCG CCA CTG CAG GGC GTG CTC GGC GGC GCC CTC ACC ATC CCT 340
C H V H Y L R P P P S R R A V L G S P R 76
TGC CAC GTC CAC TAC CTG CTG CCG CCA CCG AGC CGC CGG GCT GTG CTG GGC TCT CCG CGG 400
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V K W T F L S R G R E A E V L V A R G V 96
GTC AAG TGG ACT TTC CTG TCC CCG GGC CGG GAG GCA GAG GTG CTG GTG GCG CGG GGA GTG 460
R V K V N E A Y R F R V A L P A Y P A S 116
CGC GTC AAG GTG AAC GAG GCC TAC CGG TTC CGC GTG GCA CTG CCT CCG TAC CCA GCG TCG 520
L T D V S L A A L S E L R P N D S G I Y R 136
CTC ACC GAC GTC TCC CTG GCG CTG AGC GAG CTG CGC CCC AAC GAC TCA GGT ATC TAT CGC 580

Fig. 24A

C	E	V	Q	H	G	I	D	S	S	D	A	V	E	V	K	V	K	G	156	
TGT	GAG	GTC	CAG	CAC	GGC	ATC	GAT	GAC	AGC	AGC	GCT	GTG	GAG	GTC	AAG	GTC	AAA	GGG	640	
V	V	F	L	Y	R	E	G	S	A	R	Y	A	F	S	S	G	A	Q	176	
GTC	GTC	TTT	CTC	TAC	CGA	GAG	GGC	TCT	GCC	CGC	TAT	GCT	TTC	TCC	TTT	TCT	GGG	GCC	CAG	700
E	A	C	A	R	I	G	A	H	I	A	T	P	E	Q	L	Y	A	A	Y	196
GAG	GCC	TGT	GCC	CGC	ATT	GGA	GCC	CAC	ATC	GCC	ACC	CCG	GAG	CAG	CTC	TAT	GCC	GCC	TAC	760
L	G	G	Y	E	Q	C	D	A	G	W	L	S	D	Q	T	V	R	Y	P	216
CTT	GGG	GGC	TAT	GAG	CAA	TGT	GAT	GCT	GGC	TGG	CTG	TCG	GAT	CAG	ACC	GTG	AGG	TAT	CCC	820
I	Q	T	P	R	E	A	C	Y	G	D	M	D	G	F	P	G	V	R	N	236
ATC	CAG	ACC	CCA	CGA	GAG	GCC	TGT	TAC	GGA	GAC	ATG	GAT	GGC	TTC	CCC	GGG	GTC	CGG	AAC	880
Y	G	V	V	D	P	D	D	L	Y	D	V	Y	C	Y	A	E	D	L	N	252/361
TAT	GGT	GTG	GTG	GAC	CCG	GAT	GAC	CTC	TAT	GAT	GTG	TAC	TGT	TAT	GCT	GAA	GAC	CTA	AAT	256
G	E	L	F	L	G	D	P	P	E	K	L	T	L	E	E	A	R	A	Y	940
GGA	GAA	CTG	TTC	CTG	GGT	GAC	CCT	CCA	GAG	AAG	CTG	ACA	TTG	GAG	GAA	GCA	CGG	GCG	TAC	276
C	Q	E	R	G	A	E	I	A	T	T	G	Q	L	Y	A	A	W	D	G	1000
TGC	CAG	GAG	CGG	GGT	GCA	GAG	ATT	GCC	ACC	ACG	GGC	CAA	CTG	TAT	GCA	GCC	TGG	GAT	GGT	296
																				1060

Fig. 24B

Sequence

G	L	D	H	C	S	P	G	W	L	A	D	G	S	V	R	Y	P	I	V	316
GGC	CTG	GAC	CAC	TGC	AGC	CCA	GGG	TGG	CTA	GCT	GAT	GGC	AGT	GTG	CGC	TAC	CCC	ATC	GTC	1120
T	P	S	Q	R	C	G	G	G	L	P	G	V	K	T	L	F	L	F	P	336
ACA	CCC	AGC	CAG	CGC	TGT	GGT	GGG	GGC	TTG	CCT	GGT	GTC	AAG	ACT	CTC	TTC	CTC	TTC	CCC	1180
N	Q	T	G	F	P	N	K	H	S	R	F	N	V	Y	C	F	R	D	S	356
AAC	CAG	ACT	GGC	TTC	CCC	AAT	AAG	CAC	AGC	CGC	TTC	AAC	GTC	TAC	TGC	TTC	CGA	GAC	TCG	1240
A	Q	P	S	A	I	P	E	A	S	N	P	A	S	N	P	A	S	D	G	376
GCC	CAG	CCT	TCT	GCC	ATC	CCT	GAG	GCC	TCC	AAC	CCA	GCC	TCC	AAC	CCA	GCC	TCT	GAT	GGA	1300
L	E	A	I	V	T	V	T	E	T	L	E	E	L	Q	L	P	Q	E	A	396
CTA	GAG	GCT	ATC	GTC	ACA	GTG	ACA	GAG	ACC	CTG	GAG	GAA	CTG	CAG	CTG	CCT	CAG	GAA	GCC	1360
T	E	S	E	S	R	G	A	I	Y	S	I	P	I	M	E	D	G	G	G	253/361
ACA	GAG	AGT	GAA	TCC	CGT	GGG	GCC	ATC	TAC	TCC	ATC	CCC	ATC	ATG	GAG	GAC	GGA	GGA	GGT	416
G	S	S	T	P	E	D	P	A	E	A	P	R	T	L	L	E	F	E	T	1420
GGA	AGC	TCC	ACT	CCA	GAA	GAC	CCA	GCA	GAG	GCC	CCT	AGG	ACG	CTC	CTA	GAA	TTT	GAA	ACA	436
Q	S	M	V	P	P	T	G	F	S	E	E	E	G	K	A	L	E	E	E	1480
CAA	TCC	ATG	GTA	CCG	CCC	ACG	GGG	TTC	TCA	GAA	GAG	GAA	GGT	AAG	GCA	TTG	GAG	GAA	GAA	456
																				1540

Fig. 24C

Figure 24D

E	K	Y	E	D	E	E	K	E	E	E	E	E	E	V	E	D	476
GAG	AAA	TAT	GAA	GAT	GAA	GAG	AAA	GAG	GAA	GAA	GAG	GAG	GAG	GAG	GTG	GAG	GAT
E	A	L	W	A	W	P	S	E	L	S	S	P	G	P	E	A	496
GAG	GCT	CTG	TGG	GCA	TGG	CCC	AGC	GAG	CTC	AGC	AGC	CCG	GGC	CCT	GAG	GCC	1660
T	E	P	A	A	Q	E	K	S	L	S	Q	A	P	A	R	A	516
ACT	GAG	CCA	GCA	GCC	CAG	CAG	AAG	TCA	CTC	TCC	CAG	GCG	CCA	GCA	AGG	GCA	1720
P	G	A	S	P	L	P	D	G	E	S	E	A	S	R	P	P	536
CCT	GGT	GCA	TCA	CCA	CTT	CCT	GAT	GGA	GAG	TCA	GAA	GCT	TCC	AGG	CCT	CCA	1780
G	P	P	T	E	T	L	P	T	P	R	E	R	N	L	A	S	254/361
GGA	CCA	CCT	ACT	GAG	ACT	CTG	CCC	ACT	CCC	AGG	GAG	AGG	AAC	CTA	GCA	TCC	556
S	T	L	V	E	A	R	E	V	G	E	A	T	G	G	P	E	1840
TCC	ACT	CTG	GTT	GAG	GCA	AGA	GAG	GTG	GGG	GAG	GCA	ACT	GGT	GGT	CCT	GAG	576
V	P	R	G	E	S	E	E	T	G	S	S	E	G	A	P	S	1900
GTC	CCT	CGA	GGA	GAG	AGC	GAG	GAG	ACA	GGA	AGC	TCC	GAG	GGT	GCC	CCT	TCC	596
A	T	R	A	P	E	G	T	R	E	L	E	A	P	S	E	D	1960
GCC	ACA	CGG	GCC	CCT	GAG	GGT	ACC	AGG	GAG	CTG	GAG	GCC	CCC	TCT	GAA	GAT	616
																	2020

Fig. 24D

R T A P A G T S V Q A Q P V L P T D S A 636
 AGA ACT GCC CCA GCA GGG ACC TCA GTG CAG GCC CAG CCA GTG CTG CCC ACT GAC AGC GCC 2080

 S R G G V A V V P A S G N S A Q G S T A 656
 AGC CGA GGT GGA GTG GCC GTG GTC CCC GCA TCA GGT AAT TCT GCC CAA GGC TCA ACT GCC 2140

 L S I L L L F F P L Q L W V T * 672
 CTC TCT ATC CTA CTC CTT TTC TTC CCC CTG CAG CTC TGG GTC ACC TGA 2188

 CCTGTAGTCCTTTAAACCCACCATCATCCCAAACCTCTCCTGTCTTTGCGCTTCAATCTCTTACCCACCTCTACCTATGGG 2267

 TCTCCAATCTCGGATATCCACCTTGTGGGTATCTCAGCTCTCCGGTCTTTACCCGTGTGATCCAGCCCCGCCACTGAC 2346

 CATCTGTGACCCCTTCCCCTGCCATTGGGCCCCCTCCACCTGTGGCTCACATCTCGCCAGCCCCACAGAGCATCCTCAGGCCCT 2425
 CTCCAAGGTCCTCATCACCTATTGCAGCCCTTCAGGGCTCGGCCCTATTTTCCACTACTCCCTTCATCCGCCCTGTGTGCC 2504
 GTCCCCCTTAGCTGCCCTCCTATTGATCTCAGGGAAGCCTGGGAGTCCCTTCTCACCCCTCAACCTCCGGAGTCCAGGAG 2583
 AACCCGTACCCCCACAGAGCCTTAAGCAACTACTTCTGTGAAGTATTTTGTGACTGTTTTCATGGAAAACAAGCCTTGGA 2662
 AATAAATCTCTATTAAACCGCTTTGTAAACCAAAAAAATAAAAAAAGGGCGGCCGC 2730

Fig. 24E

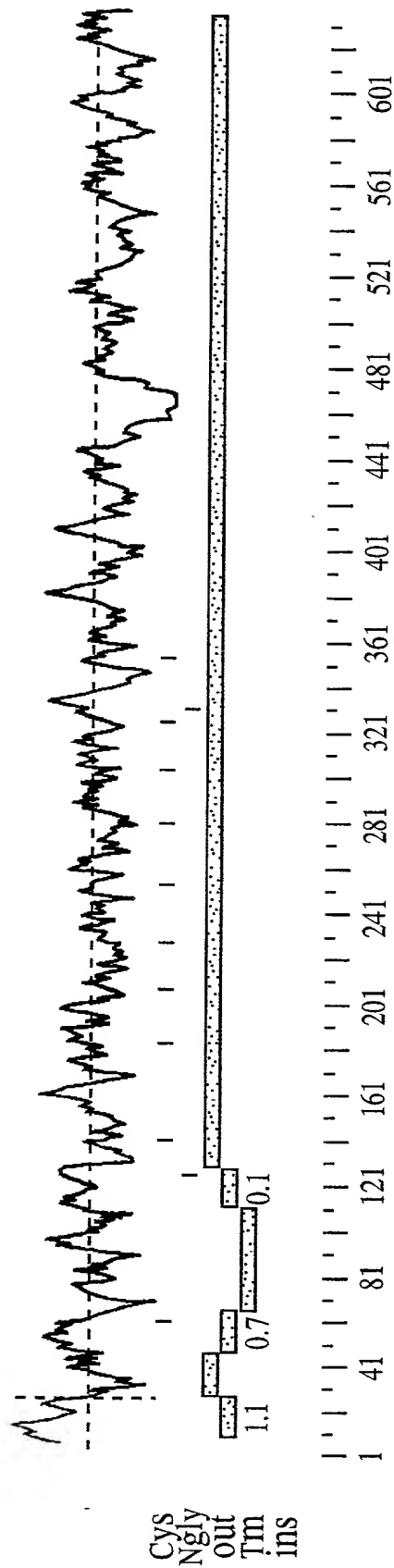


FIG. 24F

```

10      20      30      40      50      60      70
332 MAQLFLPLLAALVLAQAPAAALADVLEGDSSSEDRAFRVRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF MAQLFLPLLAALVLAQAPAAALADVLEGDSSSEDRAFRVRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRA
10      20      30      40      50      60      70

      80      90      100     110     120     130     140
332 VLGSPRVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF VLGSPRVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ
      80      90      100     110     120     130     140

150     160     170     180     190     200     210
332 HGIDSSDAVEVKVGCVFLYREGSARYAFSFGAQEACARIGAHIAATPEQLYAAAYLGGYEQCDAGWLSD
      ::::::::::::::
BEF HGIDSSDAVE-----SS
150

220     230     240     250     260     270     280
332 QTVRYPIQTPREACYGMDMGFPGRVNYGVVDPDDLVDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER
      : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF Q--RYPIQTPREACYGMDMGFPGRVNYGVVDPDDLVDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER
160     170     180     190     200     210     220

290     300     310     320     330     340     350
332 GAEIATTGQLYAAWDGGLDHCSPGWLADGSRYPPIVTPSQRCGGGLPGVKTLFLFPNQTFPNKHSRFNV
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF GAEIATTGQLYAAWDGGLDHCSPGWLADGSRYPPIVTPSQRCGGGLPGVKTLFLFPNQTFPNKHSRFNV
230     240     250     260     270     280     290

```

Fig. 24G

Fig. 24H

M	MIP	10	20	30	40	50	60	
	LLS	10	20	30	40	50	60	
	LAAL	10	20	30	40	50	60	
	VLTQ	10	20	30	40	50	60	
	APAA	10	20	30	40	50	60	
	ADDL	10	20	30	40	50	60	
	KEDS	10	20	30	40	50	60	
	SEDR	10	20	30	40	50	60	
	AFRV	10	20	30	40	50	60	
	RI-G	10	20	30	40	50	60	
	AAQL	10	20	30	40	50	60	
	RGVL	10	20	30	40	50	60	
	GAAL	10	20	30	40	50	60	
	IPCH	10	20	30	40	50	60	
	VHHL	10	20	30	40	50	60	
	PPR	10	20	30	40	50	60	
	SRRA	10	20	30	40	50	60	
H	MAQ	10	20	30	40	50	60	
	FLPL	10	20	30	40	50	60	
	LAAL	10	20	30	40	50	60	
	VLAQ	10	20	30	40	50	60	
	APAA	10	20	30	40	50	60	
	ADVL	10	20	30	40	50	60	
	EGDS	10	20	30	40	50	60	
	SEDR	10	20	30	40	50	60	
	AFRV	10	20	30	40	50	60	
	RIAG	10	20	30	40	50	60	
	DAPL	10	20	30	40	50	60	
	QGVL	10	20	30	40	50	60	
	GGAL	10	20	30	40	50	60	
	TIPCH	10	20	30	40	50	60	
	VHYL	10	20	30	40	50	60	
	RP	10	20	30	40	50	60	
	PP	10	20	30	40	50	60	
	PS	10	20	30	40	50	60	
	RRRA	10	20	30	40	50	60	
70	APG	80	90	100	110	120	130	
	FFRV	80	90	100	110	120	130	
	KWTF	80	90	100	110	120	130	
	LSGD	80	90	100	110	120	130	
	REVE	80	90	100	110	120	130	
	VLV	80	90	100	110	120	130	
	ARGL	80	90	100	110	120	130	
	RVKV	80	90	100	110	120	130	
	NEAY	80	90	100	110	120	130	
	RFRV	80	90	100	110	120	130	
	ALPAY	80	90	100	110	120	130	
	PASLT	80	90	100	110	120	130	
	DVSL	80	90	100	110	120	130	
	VLS	80	90	100	110	120	130	
	ELR	80	90	100	110	120	130	
	PND	80	90	100	110	120	130	
	SGV	80	90	100	110	120	130	
	YRCE	80	90	100	110	120	130	
	VEVQ	80	90	100	110	120	130	
H	VLG	80	90	100	110	120	130	
	SPRV	80	90	100	110	120	130	
	KWTF	80	90	100	110	120	130	
	LSRG	80	90	100	110	120	130	
	EAEV	80	90	100	110	120	130	
	LV	80	90	100	110	120	130	
	ARGV	80	90	100	110	120	130	
	RVKV	80	90	100	110	120	130	
	NEAY	80	90	100	110	120	130	
	RFRV	80	90	100	110	120	130	
	ALPAY</							

Fig. 24I

Fig. 24J

```

680      690      700      710      720      730      740
M GACYKHFSRRSWEESAESQCRAALGAHLTSICTPEEQDFVNDRYREYQWIGLNDRTIEGDFLWSDGAPLLY
H -----SI-----L-----LLF
      660

750      760      770      780      790      800      810
M ENWNPGQDSYFLSGENCVVMVWHDQQGWSQVPCNYHLSYTCCKMGLVSCGPPQPLPLAQIFGRPRRLRYAV
H -----F-----PIQ-----

820      830      840      850      860      870      880
M DTVLRYRCRDGLAQRNLPILRCQENGLWEAPQISCVPRRPGRALRSMDAPEGPRGQLSRHRKAPLTTPSS
H -----LWVT-----
      670

```

M L

H -

Fig. 24K

Fig. 24L

```

340      350      360      370      380      390      400
H CATCCCTGCCACGTCCACTACCTGCGGCCACCGCCGAGCCGCGGCTGTGCTGGCTCTCCGCGGTC
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M CATCCCATGCCACGTCCACCACTGCGGCCGCGCGCAGCCGCGGCGCGGGTTTCCCGGGGTC
310      320      330      340      350      360      370

410      420      430      440      450      460      470
H AAGTGGACTTTCCCTGTCCCGGGCGGGAGGCAGAGGTGCTGGTGGCGGGGAGTGCGCGTCAAGGTGA
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M AAGTGGACCTTCCCTGTCCGGGACCGGGAGGTAGAGGTTCTGGTGGCTCGCGGGCTGCGCGTCAAGGTAA
380      390      400      410      420      430      440

480      490      500      510      520      530      540
H ACGAGGCCTACCGGTTCCGCGTGCGACTGCCCTGCGTACCCAGCGTCGCTCACCGACGTCTCCCTGGCGCT
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M ACGAAGCCTACCGGTTCCGCGTGCGCGTGCCTACCCGCGATCGCTACGGATGTCTCTAGTATT
450      460      470      480      490      500      510

550      560      570      580      590      600      610
H GAGCGAGCTGCGCCCCAACGACTCAGGTATCTATCGCTGTGAGTCCAGCACGGCATCGATGACAGCAGC
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M GAGCGAACTGCGGGCCCAATGATTCCGGGGTCTATCGCTGCGAGTCCAGCACGGTATCGACGACAGCAGT
520      530      540      550      560      570      580

620      630      640      650      660      670      680
H GACGCTGTGGAGGTCAAGGTCAAAGGGGTGCTCTTCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCT
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M GATGCTGTGGAGGTCAAGGTCAAAGGGGTGCTCTTCTCTACAGAGAGGGCTCTGCGCGCTATGCTTTCT
590      600      610      620      630      640      650

```

Fig. 24M

```

690          700      710      720      730      740      750
H CCTTTCTGGGCCCAGGAGGCCTGTGCCCCGCAATTGGAGCCCACATCGCCACCCCGGAGAGCTCTATGC
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M CCTTCGCTGGAGCCCAGGAAGCCTGCGCTCGCATAGGAGCCCCGAATCGCCACCCCGGAGAGCTCTATGC
660      670      680      690      700      710      720

760          770      780      790      800      810      820
H CGCCTACCTTGGGGCTATGAGCAATGTGATGCTGGCTGGCTGTCTGGATCAGACCGTGAGGTATCCCATC
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M TGCCTACCTCGGCGGCTATGAGCAGTGTGATGCAGGCTGGCTGTCCGACCACAACTGTGAGGTACCCCATC
730      740      750      760      770      780      790

830          840      850      860      870      880      890
H CAGACCCCACGAGAGGCCTGTTACGGAGACATGGATGGCTTCCCCGGGTCCGGAACCTATGTTGGTGG
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M CAGAACCCACGAGAGGCCTGCTCTGGAGACATGGATGGCTATCCTGGCGTGCGGAACCTACGGAGTGGTGG
800      810      820      830      840      850      860

900          910      920      930      940      950      960
H ACCCGGATGACCTCTATGATGTGTACTGTATGCTGAAGACCTAAATGGAGAACTGTTCTGGGTGACCC
   . ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M GTCCCTGATGATCTCTATGATGTCTACTGTATGCCGAAGACCTAAATGGAGAACTGTTCTAGGCGCCCC
870      880      890      900      910      920      930

970          980      990      1000      1010      1020      1030
H TCCAGAGAAGCTGACATTGGAGGAAGCACGGCGTACTGCCAGAGCGGGGTGCAGAGATTGCCACCACG
   ::::: .. ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M TCCCAGCAAGCTGACATGGGAGGAGGCTCGGGACTACTGTCTGGAACGTGTGTGCACAGATCGCTAGCACA
940      950      960      970      980      990      1000

```

Fig. 24N

Figure 240

```

1040      1050      1060      1070      1080      1090      1100
H  GGCAACTGTATGCAGCCTGGGATGGTGGCCCTGGACCACCTGCAGCCCCAGGTGGCTAGCTGATGGCAGTG
    ::::::::::::::::::::::::::: . ::::::::::: ::::::::::: ::::::::::: :::::::::::
M  GGCCAGCTGTACGCAGCCTGGAATGGTGGCCCTGGACACAGATGTAGCCCTGGCTGGCTGGCTGATGGCAGCG
1010      1020      1030      1040      1050      1060      1070

1110      1120      1130      1140      1150      1160      1170
H  TGCCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGCTTGCCCTGGTGTCAAGACTCTCTTCCT
    ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
M  TGCCTATCCCATCATCACACCCAGCCAAACGCTGTGGGGCGGCCCTGCCAGGAGTCAAGACCCTCTTTCCT
1080      1090      1100      1110      1120      1130      1140

1180      1190      1200      1210      1220      1230      1240
H  CTTCCCCAACCAAGACTGGCTTCCCCAATAAGCACAGCCGCTTCAACGTCTACTGCTTCCGAGACTCGGCC
    ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
M  CTTTCCCCAACCAAGACTGGCTTCCCCCAGCAAGCAGAACCGCTTCAATGTCTACTGCTTCCGAGACTCTGCC
1150      1160      1170      1180      1190      1200      1210

1250      1260      1270      1280      1290      1300      1310
H  CAGCCTTCTGCCATCCCTGAGGCCCTCCAACCCAGCCTCCAACCCAGCCTCTGTATGGACTAGAGGCTATCG
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
M  CATCCCTCTGCTTCTCTGAGGCCCTCTAGCCAGCCTC-----AGATGGACTTGAGGCCATTG
1220      1230      1240      1250      1260      1270

1320      1330      1340      1350      1360      1370      1380
H  TCACAGTGACAGAGACCCCTGGAGGAACTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCCCGTGGGGC
    ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
M  TCACAGTGACAGAAAAGCTGGAGGAACTGCAGCTGCCTCAGGAAGCGATGGAGAGCGAGTCTCGTGGGGC
1280      1290      1300      1310      1320      1330      1340

```

Fig. 240

Figure 24P

```

1390      1400      1410      1420      1430      1440      1450
H CATCTACTCCATCCCATCATGGAGGACGGAGGAGGTGGAAGCTCCACTCCAGAAGACCCAGCAGAGGCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CATCTACTCCATCCCATCATTCAGAAGATGGGGGAGGAGGAAGCTCCACCCAGAAAGACCCAGCAGAGGCC
1350      1360      1370      1380      1390      1400      1410

1460      1470      1480      1490      1500      1510      1520
H CCTAGGACGCTCCTAGAAATTGAAACACAATCATGTACCGCCACGGGGTTCTCAGAAAGAGGAAGTA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCCAGGACTCCGCTAGAAATCGGAAACCAATCCATTGCACCACCTACCGAGTCCTCAGAAAGAGGAAGCGG
1420      1430      1440      1450      1460      1470      1480

1530      1540      1550      1560      1570      1580      1590
H AGGCATTGGAGGAAGAAGAGAAAATATGAAGATGAAGAAGAGAGGAGGAAGAAGAGAGGAGGT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TAGCCCTGGAGGAAGAAGAAAGATTCAAAGAC-----TTGGAGGCTCTGGAGGAAGAGAAAGAGAGCA
1490      1500      1510      1520      1530      1540

1600      1610      1620      1630      1640      1650      1660
H GGAGGATGAGGCTCTGTGGGCATGGCCAGCGAGCTCAGCAGCCCGGGCCCTGAGGCCCTCTCTCCCCACT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGAGGA-----C-CTGTGGGTGTGGCCAGAGAGCTCAGCAGCCC-----TCTCCCTACT
1550      1560      1570      1580

1670      1680      1690      1700      1710      1720
H GAGCCAGCAGCCAGGAGAAAGTCACTCTCCCAGG-----CGCCAGCAAGGGCAGTCTGCAGCCTGGTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGCTCAGAAAC---AGAGCATTCACTCTCCCAGGTGTCCCACCCAGCCAGGCAAGTCTACAGCTGGATG
1600      1610      1620      1630      1640      1650      1660

```

Fig. 24P

1730	1740	1750	1760	1770	1780	1790
H	CATCACCAC	TTCTGTATGGAGAGTCAGAA	GCTTCCAGGCTTCCAAAGG	TCCATGGACCACCTACTGAGAC		
	:::::::::					
M	CGTCACCTTCTCCTG	-----GGCCTCCAAGTTCCGTGGACCGCCTGCAGAGAC	1680	1690	1700	1710
1670						
1800	1810	1820	1830	1840	1850	1860
H	TCTGCCAC	TCCAGGAGAGGAACCTAGCATCCCCATCACCTTCCACTCTGGTTGAGGCAAGAGAGGTG				
	::: : : :	::::::::::::	::: : : :	::: : : :	::: : : :	::: : : :
M	TTTGCTCCCCCGAGGGAGTGGAGC	-----GCCACATCTACT-CC-----TGGT-GGGGCAAGAGAAAGTA	1720	1730	1740	1750
1720	1730	1740	1750	1760	1770	
1870	1880	1890	1900	1910	1920	1930
H	GGGAGGCAACTGGTGTCTGAGCTATCTGGGTCCCCTCGAGGAGAGAGCGAGAGACAGGAAGCTCC-					
	:::::::::	::: : : :	::::::::::::	::::::::::::	::::::::::::	::::::::::::
M	GGGGGGAAACTGGAGCCCTGAGCTCTCTGGGTTCCTCGA	--GAGAGCGAGGAGGCAGGAGCTCCA	1780	1790	1800	1810
1780	1790	1800	1810	1820	1830	
1940	1950	1960	1970	1980	1990	2000
H	-----GAGGGTGCCCCCTTCCCTGCTTCCAGCCACACGGGCCCTGAGGGTACCAGGGAGCTGGAGGCCCC					
	:::::::::	::::::::::::	::: : : :	::::::::::::	::::::::::::	::::::::::::
M	GCTTGGAGGATGGCCCCCTTCCCTACTTCCAGCTACATGGGCCCTGTGGTCCCAGGGAGCTGGAGACCCC					
1840	1850	1860	1870	1880	1890	1900
2010	2020	2030	2040	2050	2060	2070
H	CTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGACCTCAGTGCAGGCCCCAGCCAGTGTGCCCCACT					
	:::::::::	::: : : :	::: : : :	::::::::::::	::::::::::::	::::::::::::
M	CTCAGAAAGAGTCTGGAAGAACTGTCTTGGCAGGCACCTCAGTGCAGGCCCCAGCCAGTGTGCCCCACC					
1910	1920	1930	1940	1950	1960	1970

Fig. 24Q

Fig. 24R

Fig. 24S

Fig. 24S

```

2490      2500      2510      2520      2530
H CTTCA-TCCGCCCTGTGTGCC-----GTCC--CCTTTAGCTGC-CTCCT-----ATTGATCTC
: : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCTCAGATTTCCTGTGTACCCCGGAGGCCCTGGCCGTGCTCTGCGCTCCATGGACGCCCCAGAGGACCAC
2680      2690      2700      2710      2720      2730      2740

2540
H AGGGA-AGC-----CTGGGAGTC-CC-TTCTCACC--CCTC-AACCTCCGGAGT-CCAGGAGAAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGACAGCTCTCGAGGCACAGGAAGCACCGTTGACACCGCCCTCCAGTCTCTAGGGAGCCTGGAAGAC
2750      2760      2770      2780      2790      2800      2810

2590      2600      2610      2620      2630
H CCGTACCCCCCA-CAGAGCCTTAA-GCAACTACT-----TCT-----GTGAAGTATTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TGCTGCCCCCAGCAGGACCCCTCTCACATCAACTGCCAGTGCTCTTCCCAATGATAGGGGTGACGTGAGA
2820      2830      2840      2850      2860      2870      2880

2640      2650
H ----TTTGACTGT--TTCA-----TGGAACA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGTGGGACTGAAATTCAGAGGACAGCGCTCGAAGGGGTTTCTGGGAAACACTTGGGTGGCTCCGCCCC
2890      2900      2910      2920      2930      2940      2950

2660      2670      2680
H -----AGCCTTGGAAAT-----AAATCTCTATTAA-----AC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCACACAAGGGCCTCAGGTTTACCCCGGTAAAGTCCCTAAGTGCCTCAACTGCCCTCTCATGTCAGCTGC
2960      2970      2980      2990      3000      3010      3020

```

Fig. 24T

Sequence

```

H CGCTTTGT-----AAC-----CAAAAAAAAAAAAAA      2690      2700
: : :::::      ::::      ::::::.....:.....
M CTCCTTGTCCTCGATNTCGTNAGGGGACACTGTGCTATTTCGATCTTGATTGTCGAAGAGTTTTTAGGAT
3030      3040      3050      3060      3070      3080      3090

2710
H AAA-----AAAAAAGGGCGG--CC-----GC      2720      2730
..:      ::::::.. : : : :
M GGAGTACCAGCAAAACCAGGTGGAATAAAGTTGTCTGAACCCCAAAGAAAAA
3100      3110      3120      3130      3140      3150

```

Fig. 24U

Table 25A

M A P P A A R L A L L																11
GTCGACCCACGCTCCGCCACGCGTCCGGCCC ATG GCG CCG CCC GCC GCG CTC GCG CTC GCG CTC GCG CTC																66
S A A A L T L A A R P A P S P G L G P G																31
TCC GCC GCG GCG CTC ACG CTG GCG GCG CCC GCG CCT AGC CCC GGC CTC GGC CCC GGA																126
P E C F T A A N G A D Y R G T Q N W T A L																51
CCC GAG TGT TTC ACA GCC AAT GGT GCG GAT TAT AGG GGA ACA CAG AAC TGG ACA GCA CTA																186
Q G G K P C L F W N E T F Q H P Y N T L																71
CAA GGC GGG AAG CCA TGT CTG TTT TGG AAC GAG ACT TTC CAG CAT CCA TAC AAC ACT CTG																246
K Y P N G E G G G GGC CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA																91
AAA TAC CCC AAC GGG GAG GGG GGC CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA																306
D V S P W C Y V A E H E D G V Y W K Y C																111
GAC GTG AGC CCC TGG TGC TAT GTG GCA GAG CAC GAG GAT GGT GTC TAC TGG AAG TAC TGT																366
E I P A C Q M P G N L G C Y K D H G N P																131
GAG ATA CCT GCT TGC CAG ATG CCT GGA AAC CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA																426
P P L T G T S K T S N K L T I Q T C I S																151
CCT CCT CTA ACT GGC ACC AGT AAA ACG TCC AAC AAA CTC ACC ATA CAA ACT TGC ATC AGT																486
F C R S Q R F K F A G M E S G Y A C F C																171
TTT TGT CGG AGT CAG AGG TTC AAG TTT GCT GGG ATG GAG TCA GGC TAT GCT TGC TTC TGT																546

Fig. 25A

G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GGA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	CTG	CTG	CCA	CAG	GAG	AGG	1026

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Fig. 25B

P	A	V	N	Q	T	V	A	E	V	I	T	E	Q	A	N	L	S	V	S	351
CCC	GCT	GTC	AAC	CAG	ACG	GTG	GCC	GAG	GTG	ATC	ACG	GAG	CAG	GCC	AAC	CTC	AGT	GTC	AGC	1086
A	A	R	S	S	K	V	L	Y	V	I	T	T	S	P	S	H	P	P	Q	371
GCT	GCC	CGG	TCC	TCC	AAA	GTC	CTC	TAT	GTC	ATC	ACC	ACC	AGC	CCC	AGC	CAC	CCA	CCT	CAG	1146
T	V	P	G	S	N	S	W	A	P	P	M	G	A	G	S	H	R	V	E	391
ACT	GTC	CCA	GGT	AGC	AAT	TCC	TGG	GCG	CCA	CCC	ATG	GGG	GCT	GGA	AGC	CAC	AGA	GTT	GAA	1206
G	W	T	V	Y	G	L	A	T	L	L	I	L	T	V	T	A	I	V	A	411
GGA	TGG	ACA	GTC	TAT	GGT	CTG	GCA	ACT	CTC	CTC	ATC	CTC	ACA	GTC	ACA	GCC	ATT	GTA	GCA	1266
K	I	L	L	H	V	T	F	K	S	H	R	V	P	A	S	G	D	L	R	431
AAG	ATA	CTT	CTG	CAC	GTC	ACA	TTC	AAA	TCC	CAT	CGT	GTT	CCT	GCT	TCA	GGG	GAC	CTT	AGG	1326
D	C	H	Q	P	G	T	S	G	E	I	W	S	I	F	Y	K	P	S	T	451
GAT	TGT	CAT	CAA	CCA	GGG	ACT	TCG	GGG	GAA	ATC	TGG	AGC	ATT	TTT	TAC	AAG	CCT	TCC	ACT	1386
S	I	S	I	F	K	K	K	L	K	G	Q	S	Q	Q	D	D	R	N	P	471
TCA	ATT	TCC	ATC	TTT	AAG	AAG	AAA	CTC	AAG	GGT	CAG	AGT	CAA	CAA	GAT	GAC	CGC	AAT	CCC	1446
L	V	S	D	*																476
CTT	GTG	AGT	GAC	TAA																1461

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Fig. 25C

AAACCCCACTGTGCCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGTCTCTC 1540
 TGACAGACTCTTCCCTCCTCTCCCTCTGCTCCCTCGGCTCTTGGGGAACCTCTCCTCTACAGACTAGGAAGAGGCACCT 1620
 GCTGCCAGGGCAGGACAGCCTGGATTCTCTCTGCTT 1657

Fig. 25D

GTCGACCCACGGCTCCGCCGGCTCCCGGTGCTGCCCTCTGCCCCGGCCGGGGGTCCCCGCACTGACGGCC 79
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M A P A P A A R L A L L S A A A L T L A 19
 C ATG GCG CCG CCC GCC GCG CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137

A R P A P G P R S G P E C F T A N G A D 39
 GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197

Y R G T Q S W T A L Q G G GGT GGG AAG CCA TGT CTG TTC TGG AAC 257
 TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC

E T F Q H P Y N T L K Y P N G E G L G 79
 GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA CTG GGC 317

E H N Y C R N P D G D V S P W C Y V A E 99
 GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

Fig. 25E

H E D G V Y W K Y C E I P A C Q M P G N 119
CAT GAG GAC GGA GTC TAC TGG AAG TAC TGT GAA ATT CCT GCC TGC CAG ATG CCT GGA AAC 437

L G C Y K D H G N P P P L T G T S K T S 139
CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA CCT CCT CTC ACG GGC ACC AGT AAA ACC TCT 497

N K L T I Q T C I S F C R S Q R F K F A 159
AAC AAG CTC ACC ATA CAA ACC TGT ATC AGC TTC TGT CGG AGT CAG AGA TTC AAG TTT GCT 557

G M E S G Y A C F C G N N P D Y W K H G 179
GGG ATG GAG TCA GGC TAT GCC TGC TTC TGT GGG AAC AAT CCT GAC TAC TGG AAG CAC GGG 617

E A A S T E C N S V C F G D H T Q P C G 199
GAG GCG GCC AGC ACC GAG TGC AAT AGT GTC TGC TTC TGC GGG GAC CAC ACG CAG CCC TGC GGT 677

G D G R I I L F D T L V G A C G G N Y S 219
GGG GAC GGC AGG ATT ATC CTC TTT GAC ACT CTC GTG GGC GCC TGC GGT GGG AAC TAC TCA 737

A M A A V V Y S P D F P D T Y A T G R V 239
GCC ATG GCA GCC GTG GTG TAC TCC CCT GAC TTC CCT GAC ACC TAC GCC ACT GGC AGA GTC 797

C Y W T I R V P G A S R I H F N F T L F 259
TGC TAC TGG ACC ATC CGG GTT CCA GGA GCC TCT CGC ATC CAT TTC AAC TTC ACC CTG TTT 857

D I R D S A D M V E L L D G Y T H R V L 279
GAT ATC AGG GAC TCT GCA GAC ATG GTG GAG CTG CTG GAC GGC TAC ACC CAC CGC GTC CTG 917

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Fig. 25F

V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	299
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	TTC	AAT	GTC	TCT	CTG	GAT	TTT	GTC	977
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	319
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TTG	TAC	CAA	1037
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	339
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	399
CAG	TTG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	CCA	TCT	TTA	AGA	AGA	AGC	TCA	AGG	1457

Fig. 25G

V R V N K M T A I P S * 471
GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA 1493

GTGACTGAAGCCACGCCCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCTGAGTTCTCCTCTGATGAGTTC 1572
CCTGCCCTTCCCATTCACCAACCATCTCTTTTGGAGCACCCCTGCTTTAGAGGCAGCCCCAGCCTGGGATCCTCCATCACAT 1651
GTACCAGCCTGGCTGCTCTGCTGGGATGGTAAGACAGAGCCAGGCTGACAGACAGCTGGACCTGACTCCAGAAGA 1730
CTCTTGGTGGTGGGAGGTATAGTGTAGGATGAGTTTCTTGTCTTCTCTGTTTGTCCACATACAGATCGGTTTC 1809
CCCTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTACAGTTTCTAGGCTGGCCTGGTTCCCCACTAAGA 1888
GTGGCATTTGGGCCCCAGAGGCCAGAGCCCCAGTGTAGGCTTTTCTGCTGCCAACTACCATGTGTCACT 1967
AGTCCAGGGGACTGAGAGCAGGGCCACACAGATGTCACTTTCTAGAGGTTCTTTTAGTACCCACTGACCAATGG 2046
GGCAAGCCTGAGGATTGGTCCATCTGTTTGTCCATGGAAACAGACACAGTGAACCTCCTGGATACTAGACTTAACTAGCC 2125
TAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAAATCAGCCTGTCTTCTGCTCAGCCCCAAGCCTGTAGCCTAG 2204
AGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAGCCTAGAGC 2283
TGGGCTGTAGCACAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAGCACAGAGCTGG 2362
GGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAACTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441
GACCCTAGGTTCTATCCCAGCACTATCAGAAAGTGGAGAGAAAAGACTGCACCATAGCATGGGCAGCATCTGTGG 2520
TTCCTACGTGAGGTGCATCATTTTAAAGCAGATCAAAACTACCGGAGTTTGTCTTGTCCCTTATCATGGGAGC 2599
AGAGTAGGAGTAAGGGCTCTGGTCTTGCTCATTTGCTCCACAGAGGAGGAGGAAAGGTCAGGCTTGGGAACCTGGA 2678
GATCCTCCCAGGAAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAGGCCATCCCCGACTGAGAAATC 2757
CTGCAGTCTGGAAGTGCCCTTTGTAGCAGCAGCTGTGCCCTGAAGGTAGACCTTGGTCACCTCCTGCCAGCCCTTGA 2836
GCCCTGCTCTCCTGGGTACCCCTCCTGGAACACCATGCTAACTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCCTC 2915
TCCCTAGCTGCTGCCAGGACTGTCTGGGCCCATCTGGGATCAGGGAGAGGAGGAGGAGTACTGACGAGGCAG 2994
TGACCTGAGCTGATGATCAACAGAGGACACAGAGTCTACAGTGGCTGGCTGCTGCTCAGCTCCTATGGGAGGCC 3073
TACAGGGGTACTAAGCTAGGGGTCTCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152
CACTACATAAGAAAGACCACCTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC 3231

Fig. 25H

CCTGAGACCAAGTTGAGTCACAGAGTGCCATGTGCGTAGTGCAATAAGGATATGGGTTCTTAACCAGGGAAGGCTC 3310
 ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACTCACCTGTCTCTTCCT 3389
 ATCTCGACACAGGAAGCAAGCCCCAGTGTGTGGCAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468
 TGCCACCGTCCCTTTTGTGTGGCCTGGCACAGCCCCAACACTGCAGGGCCCACTTCTCTTTGGGGGTAGGGACAC 3547
 ATAAGGAAAACATAACCCACCTCCAAACAGCAGAGGACAGTGGGAAGGAGGCTGTAAATCACCCAGGCCAGACCTC 3626
 CAGAAATGACAGGCACAGTCTGTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGGTAACACCCCTGCCCTG 3705
 GAGCATAGGGTAAGCCGAGGAGAGAGCAGCCCTCAGAGACATCAGCTAAAACATAGGTGCCCTATGTCCCTCCCT 3784
 TCCTGTCACACTGCTTACAAAGCAGACAGAGTAGGAAAGAGGTCTTCATCCTCTCCACATCAGCAAGGATAGGGCT 3863
 GCGGCTGCCATAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942
 AAAGCTCTTGAAGATCAAAAGCTCTGGCGGTACAGCTGTCCCTGTGGCCAGCCCATGGGATGTGCCCTGGGCCAG 4021
 GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCCACTGATGCTCCTCATCATCCGCTGGCCTGACACTATCA 4100
 GAGCTCGCGCCGCTGTTGCCAGGCAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGAATGGCCTCCAGA 4179
 CTCTGTCAGCCTCTGCAGGGCCACACAAGTCTCCGAGGCCAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCCTCCT 4258
 GTGGAGTGCTCCTGTTGATGCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACCTGCTAACCTCCGATTTGGTCCCTTGT 4337
 GTCCTGTTTACTGCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTCTGGAGTGGGGGTGGGATGCT 4416
 GGCTGCACCCCCACCTGGTCTGCCAACAGAACCTGGGGGCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495
 ACACTGGCCAGGCTGAGTGGGCAGAGCAAAACAAGTGAAGGGATCTCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574
 AGATCCAGCGAGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAAATCTCACCCCTCCAGCAG 4653
 GGATATGACTTTGGACAACAAGGCTTTATTTGTAATAATGCTCTTAATATGCAACTTTGAGAAATAAGATAGAAACATCA 4732
 TGTATTTTAAAAATATAAAATGAAGTGTGACACACTGTATACAATTTAAATATATATTTTAGGATTTTGTATTAAAGAA 4811
 AATGGAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAAATGTTATTTTACTGTTTGAAGAAAAATAATATTCTCA 4890
 TTGTTGTAGAAAAAATAAAAAAAGGGCGGCCG 4928

Fig. 25I

Fig. 25J

Fig. 25K

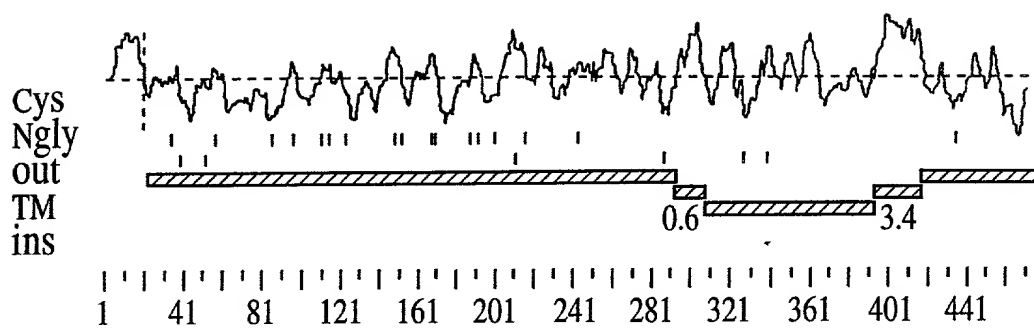


Fig. 25L

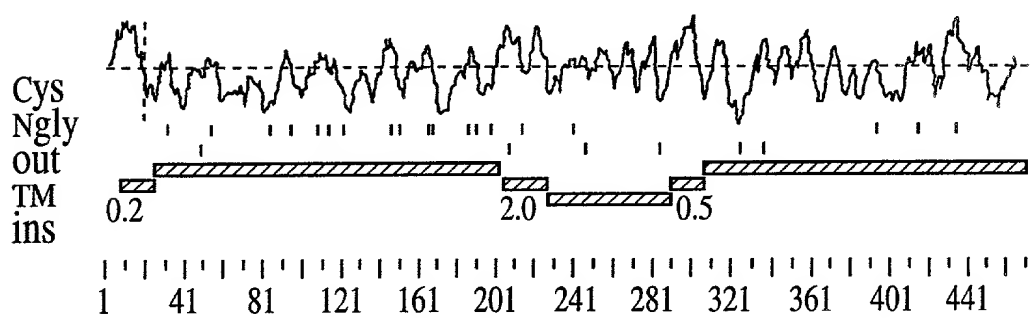


Fig. 25M

[illegible]

Fig. 26A

G L R L V D G N S C S G R V E V K F Q 173
 GGT TTG AGG CTA GTG GAT GGA AAC AAC TCC TGT TCA GGG AGA GTG GAG GTG AAA TTC CAA 546

 E R W G T I C D D G W N L N T A A V V C 193
 GAA AGG TGG GGG ACT ATA TGT GAT GAT GGG TGG AAC TTG AAT ACT GCT GCC GTG GTG TGC 606

 R Q L G C P S S F I S S G V V N S P A V 213
 AGG CAA CTA GGA TGT CCA TCT TCT TCT TTT ATT TCT TCT GGA GTT GTT AAT AGC CCT GCT GTA 666

 L R P I W L D D I L C Q G N E L A L W N 233
 TTG CGC CCC ATT TGG CTG GAT GAT GAC ATT TTA TGC CAG GGG AAT GAG TTG GCA CTC TGG AAT 726

 C R H R G W G N H D C S H N E D V T L T 253
 TGC AGA CAT CGT GGA TGG GGA AAT CAT GAC TGC TGC AGT CAC AAT GAG GAT GTC ACA TTA ACT 786

 C Y D S S D L E L R L V G G T G G A C T T G T A G G T G G A C T A C T A A C C G C T G T A T G G G G 846
 TGT TAT GAT AGT AGT GAT CTT GAA CTA AGG CTT GTA GGT GGA ACT AAC AAC CGC TGT ATG GGG

 R V E L K I Q G R W G T V C H H K W N N 293
 AGA GTA GAG CTG AAA ATC CAA GGA AGG TGG GGG ACC GTA TGC TGC CAC CAT AAG TGG AAC AAT 906

 A A A D V V C K Q L G C G T A L H F A G 313
 GCT GCA GCT GAT GTC GTA TGC AAG CAG TTG GGA TGT GGA ACC GCA CTT CAC TTC GCT GGC 966

 L P H L Q S G S D V V W L D G V S C S G 333
 TTG CCT CAT TTG CAG TCA GGG TCT GAT GTT GTA TGG CTT GAT GGT GTC TCC TGC TCC GGT 1026

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Fig. 26B

N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	T	I	393	
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

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Fig. 26C

C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	533
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
ACC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	CCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	CTC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106

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Fig. 26D

G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTG	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226
G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	CTT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646

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Fig. 26E

C P I V Q H P E D T C I H S R E V G V 893
TGC CCC ATT GTT CAA CAT CCG GAA GAC ACT TGT ATC CAC AGC AGA GAA GTT GGA GTT GTC 2706

C S R Y T D V R L V N G K S Q C D G Q V 913
TGT TCC CGA TAT ACA GAT GTC CGA CTT GTG AAT GGC AAA TCC CAG TGT GAC GGG CAA GTG 2766

E I N V L G H W G S L C D T H W D P E D 933
GAG ATC AAC GTG CTT GGA CAC TGG GGC TCA CTG TGT GAC ACC CAC TGG GAC CCA GAA GAT 2826

A R V L C R Q L S C G T A L S T T G G K 953
GCC CGT GTT CTA TGC AGA CAG CTC AGC TGT GGG ACT GCT CTC TCA ACC ACA GGA GGA AAA 2886

Y I G E R S V R V W G H R F H C L G N E 973
TAT ATT GGA GAA AGA AGT GTT CGT GTG TGG GGA CAC AGG TTT CAT TGC TTA GGG AAT GAG 2946

S L L D N C Q M T V L G A P P C I H G N 993
TCA CTT CTG GAT AAC TGT CAA ATG ACA GGA AGC CTT GGA GCA CCT CCC TGT ATC CAT GGA AAT 3006

T V S V I C T G S L T Q P L F P C L A N 1013
ACT GTC TCT GTG ATC TGC ACA GGA AGC CTG ACC CAG CCA CTG TTT CCA TGC CTC GCA AAT 3066

V S D P Y L S A V P E G S A L I C L E D 1033
GTA TCT GAC CCA TAT TTG TCT GCA GTT CCA GAG GGC AGT GCT TTG ATC TGC TTA GAG GAC 3126

K R L R L V D G D S R C A G R V E I Y H 1053
AAA CGG CTC CGC CTA GTG GAT GGG GAC AGC CGC TGT GCC GGG AGA GTA GAG ATC TAT CAC 3186

Fig. 26F

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D G G F W G T I C D D G G D L S D A H V V 1073
GAC GGC TTC TGG GGC ACC ATC TGT GAT GAC GGC TGG GAC CTG AGC GAT GCC CAC GTG GTG 3246

C Q K L G C G V A F N A T V S A H F G E 1093
TGT CAA AAG CTG GGC TGT GGA GTG GCC TTC AAT GCC ACG GTC TCT GCT CAC TTT GGG GAG 3306

G S G P I W L D D L N C T G T E S H L W 1113
GGG TCA GGG CCC ATC TGG CTG GAT GAC CTG AAC TGC ACA GGA ACG GAG TCC CAC TTG TGG 3366

Q C P S R G W G Q H D C R H K E D A G V 1133
CAG TGC CCT TCC CGC GGC TGG GGG CAG CAC GAC TGC AGG CAC AAG GAG GAC GCA GGG GTC 3426

I C S E F T A L R L Y S E T E T E S C A 1153
ATC TGC TCA GAA TTC ACA GCC TTG AGG CTC TAC AGT GAA ACT GAA ACA GAG AGC TGT GCT 3486

G R L E V F Y N G T W G S V G R R N I T 1173
GGG AGA TTG GAA GTC TTC TAT AAC GGG ACC TGG GGC AGC GTC GGC AGG AGG AAC ATC ACC 3546

T A I A G I V C R Q L G C G E N G V V S 1193
ACA GCC ATA GCA GGC ATT GTG TGC AGG CAG CTG GGC TGT GGC GAG AAT GGA GTT GTC AGC 3606

L A P L S K T G S G F M W V D I Q C P 1213
CTC GCC CCT TTA TCT AAG ACA GGC TCT GGT TTC ATG TGG GTG GAT GAC ATT CAG TGT CCT 3666

K T H I S I W Q C L S A P W E R R I S S 1233
AAA ACG CAT ATC TCC ATA TGG CAG TGC CTG TCT GCC CCA TGG GAG CGA AGA ATC TCC AGC 3726

Fig. 26G

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

Fig. 26H

C	L	K	R	E	D	P	H	G	T	R	T	S	D	D	T	P	N	H	G	1433
TGC	CTC	AAG	AGA	GAG	GAC	CCA	CAT	GGG	ACA	AGA	ACC	TCA	GAT	GAC	ACC	CCC	AAC	CAT	GGT	4326
C	E	D	A	S	D	T	S	L	L	G	V	L	P	A	S	E	A	T	K	1453
TGT	GAA	GAT	GCT	AGC	GAC	ACA	TCG	CTG	TTG	GGA	GTT	CTT	CCT	GCC	TCT	GAA	GCC	ACA	AAA	4386
*																				1454
TGA																				4389
CTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACAACAACCTTTAAATGAATAAAGAGGA																				4468
AGTCAAGTTGCCCTATGGAAAACCTTGTCCAAATAACATTTCTTGAACAATAGGAGAAACAGCTAAATTTGATAAAAGACTGG																				4547
TGATAATAAAAAATTGAATTATGTATATCACTGTTAAAAAATAAAAAAAAAAAAAAAAAACGGACGCGTGGGTCG																				4626
AC																				4628

Fig. 26I

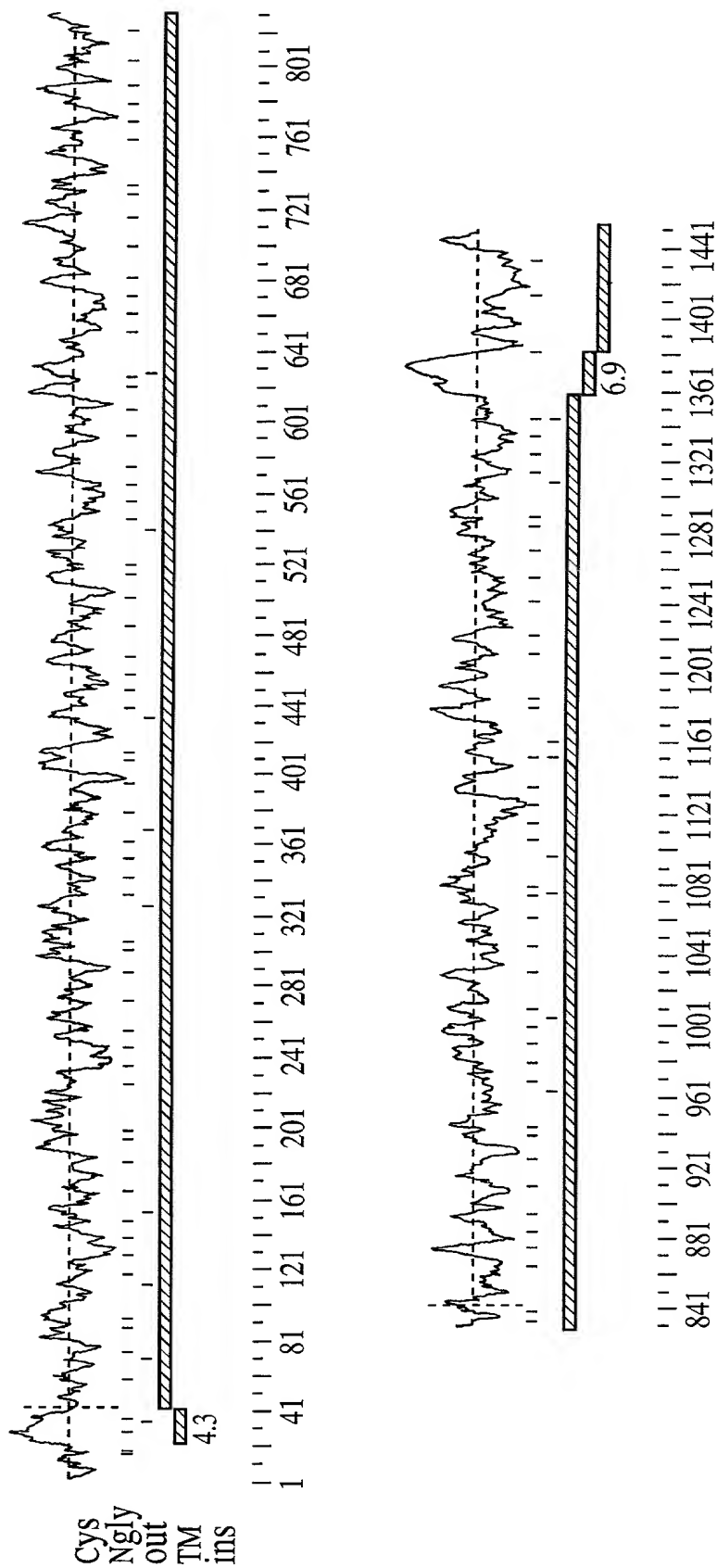


Fig. 26J

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10      20      30      40      50      60      70
Hum.  MMLPQNSWHIDFGRCCHQNLFSAVVTICILLNSCFLISSFNGTDLELRLVNGDGPCSGTVEVKFQGQWG
      ::      ::      ::      ::      ::      ::      ::
WC1  MAL-----GR---HLSLRGL---CVLLLGTL---MVG---GQALELRLKDGVHRCCEGRVEVKHQGEWG
      10      20      30      40      50

      80      90      100     110     120     130
Hum.  TVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQH---REWGSHN
      ::      ::      ::      ::      ::      ::      ::
WC1  TVDGYRWTLKDASVVCRCQLGCGAAIG-FPGGAYFGPGLPIWLLYTSCEGTESTVSDCEHSNIKDYRNDG
      60      70      80      90     100     110

      140     150     160     170     180     190     200
Hum.  CYHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLTAAVVCRCQLGCPSSFISG
      ::      ::      ::      ::      ::      ::      ::
WC1  YNHGRDAGVVCSG-----FVRLAGGDGPCSGRVEVHSGEAWIPVSDGNFTLATAQIICAELGCGKAVSVLG
      120     130     140     150     160     170     180

      210     220     230     240     250     260     270
Hum.  VVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTICYDSSDLELRLVGTNRCMGRVE
      .      .      .      .      .      .      .
WC1  HELFRESSAQVWAEFFRCEGEPELWVCPRVPCPGTCHHSGSAQVVC SAYSEVRL-MTNGSSQCEGQVE
      190     200     210     220     230     240     250
```

Fig. 26K

	280	290	300	310	320	330	340
Hum.	LKIQRWGT	CHHKWN	AAADVCK	QLGCGT	ALHFAGL	PHLQSG	SDVVWLDG

WC1	MNISQWR	ALCASH	WLANAN	VICRQL	GCGVAI	STPGPH	LVVEGDQI
	260	270	280	290	300	310	320
	350	360	370	380	390	400	410
Hum.	VNFDCL	HQNDV	SICSDG	ADLELR	ADGSNN	CSGRVE	RIHEQW

WC1	GGPDC	SHGNT	ASVICS	-GNQI	-----	QVLPQC	ND-----
	330	340					350
	420	430	440	450	460	470	480
Hum.	FGSRR	AKPSNE	ARDIWI	NSISCT	GNESAL	WDCTYD	GKAKRT

WC1	-----	SQPTGS	A-----	ASEDSA	---PY	-----	CSDSRQ
		360				370	380
	490	500	510	520	530	540	550
Hum.	GRLEV	KYQGE	WTVCH	DRWST	RNAAV	VCKQLG	CGKPMH

WC1	GRVEI	LDQGS	WGTIC	DDGWD	LDARV	VCRQLG	CGEALN
	390	400	410	420	430	440	450

Fig. 26L

Hum.	560	570	580	590	600	610	620
	HS	GW	GK	HN	CV	HRE	DV
	I	V	T	C	S	G	D
	A	T	W	G	L	R	L
	V	G	S	N	R	C	S
	G	R	L	E	V	F	Q
	G	R	W	G	T	V	C
	D	D	G	W	N	S	K
	A	A	A	V	V	C	S
	Q	L	D	C			
WC1	460	470	480	490	500	510	520
	S	R	G	W	G	H	N
	C	R	H	K	Q	D	A
	G	I	C	S	--	E	F
	L	A	R	M	V	S	E
	D	Q	C	A	G	W	L
	E	V	F	Y	N	G	T
	W	G	S	V	C	R	N
	P	M	E	D	I	T	V
	S	T	I	C	R	L	G
Hum.	630	640	650	660	670	680	690
	P	S	S	I	I	G	M
	G	L	N	A	S	T	G
	Y	G	K	I	W	L	D
	D	V	S	C	D	E	S
	D	L	W	S	C	R	N
	S	G	W	G	N	N	D
	C	S	H	E	D	V	G
	V	I	C	S	D	A	S
	D	M	E	L	R	L	V
	G	G	S				
WC1	530	540	550	560	570	580	590
	G	D	S	G	T	L	N
	S	S	V	A	L	R	E
	G	F	R	P	Q	W	D
	R	I	Q	C	R	K	T
	D	T	S	L	W	Q	C
	P	S	D	P	W	N	Y
	N	S	C	S	P	K	E
	E	A	I	W	C	A	D
	S	R	--	Q	I	R	L
	V	D	G	G			
Hum.	700	710	720	730	740	750	760
	S	R	C	A	G	K	V
	E	N	V	N	Q	G	A
	V	G	I	L	C	A	N
	G	M	N	I	A	E	V
	V	C	R	L	E	C	G
	S	A	I	R	V	S	R
	E	P	H	F	T	E	R
	T	L	H	I	L	M	S
	N	S	G	T	G	G	E
	A	S	L				
WC1	600	610	620	630	640	650	660
	G	R	C	S	G	R	V
	E	I	L	D	Q	G	S
	G	T	I	C	D	D	R
	W	D	L	D	A	R	V
	V	C	K	L	G	C	E
	A	L	D	A	T	V	S
	S	F	F	G	T	G	S
	G	P	I	W	L	D	E
	V	N	C	R	G	E	E
	S	Q	V				
Hum.	770	780	790	800	810	820	830
	W	D	C	I	R	W	E
	K	Q	T	A	C	H	L
	N	M	E	A	S	L	I
	C	S	A	H	R	Q	P
	R	L	V	G	A	D	M
	P	C	S	G	R	V	E
	K	H	A	D	T	W	R
	S	V	C	D	S	D	F
	S	L	H	A	N	V	L
	C	R	E	L			
WC1	670	680	690	700	710	720	730
	W	R	C	P	S	W	G
	R	Q	H	N	C	N	H
	Q	E	D	A	G	V	I
	C	S	G	F	--	V	R
	L	A	G	G	D	G	P
	C	S	G	R	V	E	H
	S	G	E	A	W	T	P
	V	S	D	G	N	F	T
	L	P	T	A	Q	V	I
	C	A	E	L			

Fig. 26M

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840      850      860      870      880      890      900
Hum.  NCGDAISLSVGDHFGKGNGLTWAEEKFQCEGSETHALCPIVQHPEDTCIHSREVGVCSTRYTDVRLV-NG
      :: :::: : :: :::: ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :
WC1   GCGKAVSVLGHMPFRESDGQVWAEFFRCDCGGEPELWSCPRVPCGGTCLHSGAAQVVCVSVYTEVQLMKNG
      740      750      760      770      780      790      800

910      920      930      940      950      960      970
Hum.  KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGKYGIGERSVRVWGHFRFHCIGNESL
      ::::: ::::: ::::: ::::: ::::: ::::: : : : : ::::: ::::: :::::
WC1   TSQCEGQVEMKISGRWRALCASHWSLANANVVCRLGCGVAISTPRGPHLVEGDDQISTAQFHCSGAESEF
      810      820      830      840      850      860      870

980      990      1000     1010     1020     1030     1040
Hum.  LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRC
      : ::::: ::::: : ::::: ::::: : ::::: ::::: : ::::: ::::: :
WC1   LWSCPVTALGGPDCSHGNTASVICSGNHTQVLPQCNDFLSQPAGSAASEESSPYCSDSRQLRLVDGGGPC
      880      890      900      910      920      930      940

1050     1060     1070     1080     1090     1100     1110
Hum.  AGRVEIYHDGFWGTICDDGWDLSDAHVVQCQLGCGVAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQC
      ::::: : ::::: ::::: ::::: ::::: ::::: : ::::: ::::: ::::: : :::::
WC1   GGRVEILDQGSWGTICDDDWLDDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDDLNCTGKESHVWRC
      950      960      970      980      990      1000     1010

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Fig. 26N

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1120      1130      1140      1150      1160      1170      1180
Hum.  PSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRNITTAIAGIVCRQLG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  PSRGWGRHDCRHKEDAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLG
      1020      1030      1040      1050      1060      1070

1190      1200      1210      1220      1230      1240
Hum.  CGENGVS LAPLSKTGSGFMWVD DIQCPKTHISIWQCL SAPWERRISSPAEETWITCEDR-----
      : : : : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CGDGS LNTSVGLREGSRPRWVD LIQCRKMDTSLWQCPSGPWKYSSCSPKEEAYISCEGRRPKSCPTAAA
      1080      1090      1100      1110      1120      1130      1140

1250      1260      1270      1280      1290      1300
Hum.  -----IRVRGGDTECSGRVEIWHAGSWGTVCDSDWDLAEAEVVCQQLGCGSALAAALRDASFQGTGTIW
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CTDREKLRLRGDSECSGRVEVWHNGSWGTVCDSDWSLAEAEVVCQQLGCGQALEAVRSAAAFGPGNGSIW
      1150      1160      1170      1180      1190      1200      1210

1310      1320      1330      1340      1350      1360
Hum.  LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG-----QSLKSLNASSGHLALI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  LDEVQC GGRESLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTAGTRTTSNLSLPGIFSLPGVLC LI
      1220      1230      1240      1250      1260      1270      1280

```

Fig. 260

```

1370      1380      1390      1400      1410
Hum.  LSSIFGLLLVLFILTWCRVQK-----QKHLPLRVS-----TRRRG-----SLEENLFHEME
      :...: :...: . : : :...: . : : :...: . : : :...:
WC1  LGSLLFLVLVILVTQLLRW-RAERRALSSYEDALAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAE
1290      1300      1310      1320      1330      1340      1350

      1420      1430      1440
Hum.  TC-----LKREDPHGTRTSD-----DTPNHGCEDAS-----DTSLLGV
      . : : :...: . : : :...: . : : :...:
WC1  EVPVGTPSPSQNGEEEEVPPEKEDGVRSSQTGSFLNFSREANPGEEESFWLLQKKGDAGYDDVELSA
1360      1370      1380      1390      1400      1410      1420

      1450
Hum.  LPASEAT-K
      : : :
WC1  LGTSPVTFS
1430

```

Fig. 26P

Fig. 26Q-1

```

280      290      300      310      320      330      340
Hum. TCCTTCGCCATGTTTCGTTTGGACAAGCCGTGA--CTAGACATGGAAAAATTGGCTTGATGATGTTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GCCATTG--GTTTTCCTGGAGGGGCTTATTTTGGGCCAGGACTTGGCCCCCATTTGGCTTTTGTATACTTC
220      230      240      250      260      270      280
      350      360      370      380      390      400      410
Hum. CTGTTATGGAATGAGTCAGCTCTCTGGGAATGTCAACACCCGGGAATGGGGAAGCCATAACTGTTATCAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGTGAAGGACAGAGTCAACTGTGAGTGTGAGCAT-TCTAATATTAAAGAC-TATC-GTAATGAT
290      300      310      320      330      340      350

420      430      440      450      460      470      480
Hum. GGAGAAGATGTTGGTGTGAACGTGTTATGTTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GGCTATAATCATGGTCGGGA---TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
360      370      380      390      400      410      420

490      500      510      520      530      540      550
Hum. AACTCCTGTTCAAGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GAC-CCTGCTCAGGGCGAGTAGAAGTGCAATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT
430      440      450      460      470      480

```

Fig. 26Q-2

	560	570	580	590	600	610	620
Hum.	ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTATTCTTCTGGAGTTGT						
	490	500			510		520
WC1	TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG						
Hum.	630	640	650	660	670	680	690
	TAATAGCCCTGCTGTATTGCGCCCATTTGGCTGGATGACATTTATGCCAGGGAATGAGTTGGCACT-						
WC1	TTGTGGC-----AAGGCTG--TGCTGT-----CCTGGGACATGAG----CTCTT						
	530		540		550	560	
Hum.	700	710	720	730	740	750	760
	CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT						
WC1	CAGAGAGTCCAGT-GCC-----CAGGTCTG--GGC---TGAAGAGTTCA-----GG						
	570	580		590	600		
Hum.	770	780	790	800	810	820	830
	TATGATAGTAGTGATCTTGAACTAAGGCTTGTAGGTGGAACCTAACCGCTGTATGGGAGAGTAGAGCTGA						
WC1	TGTGAGGGGGAGGAGCCTGAGCT---CT-----GGGTCTGCC--CAGAGTG-----CCCTG-						
	610	620	630		640		650

Fig. 26Q-3

```

      840      850      860      870      880      890      900
Hum.  AAATCCAAGGAGGTGGGGACCGTATGCCACCATAAGTGAACAATGCTGCAGCTGATGTCGTATGCAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ---TCCA-----GGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT
      660      670      680      690      700

      910      920      930      940      950      960      970
Hum.  GCAGTTGGGATGTGGAACCGCACTTCACCTTCGCTGGCTTGCCCTCATTTGCAGTCAGGGTCTGATGTGTA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ACT-----CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCCTC-TCAG-TGTGAAGGGCAGGTGGAGAT
      710      720      730      740      750      760

      980      990      1000      1010      1020      1030      1040
Hum.  TGGCTTGATGGTGTCTCCTGCTCCGGTAATGAATCTTTCTTTGGGACTGCAGACATTCGGGAACCGTCA
      . . . . . : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GAACATT-----TCTG-GACAATGGAGAGCGCTCTGTGCCCTCCC-ACTGGAGTCTGGCCAAATGCC---A
      770      780      790      800      810      820

      1050      1060      1070      1080      1090      1100      1110
Hum.  ATTTTGACTGTCTTCATCAAAAACGATGTCTGTGATCTGCTCAGATGGAGCAGATTGGAACCTGCGACT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGTTATCTGTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT
      830      840      850      860      870      880

```

Fig. 26Q-4

```

1120      1130      1140      1150      1160      1170      1180
Hum.  AGCAGATGGAAGTAACAATTGTTCAAGGAGAGTAGAGGTGAGAAATTCA-TGAACAGTGGTGGACAAATATG
      :: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::
WC1  TG---GTGGAAGAAG---GTGATCAG--ATCCTAACAGCCCCGATTTCACGTGCTCTG---GGGC-----TG
      890      900      910      920      930

1190      1200      1210      1220      1230      1240      1250
Hum.  TGACCAGAACTGGAAGAAATGAACAAGCCCTTGTGTTTGTAGCAGCTAGGATGTCCGTTCAGCGTCTTT
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::
WC1  AGTCCT-TCCTGTGGAGTTGT-----CCT-GTGACT-----GCC-CTGGGTGTCCTGACTGTTTCCCAT
      940      950      960      970      980      990

1260      1270      1280      1290      1300      1310      1320
Hum.  GGCAG-TCGTCTGTCTAAACCTAGTAATGAAGCTAGAGACATTTGGATAAACAGCATAATCTTGCACTGGG
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::
WC1  GGCAACACAGCCCTCTGTGATCTGCTCAGGAAACCAGATCCAGGTGCTTCCCCCAGTGCAACGA-CTCCG--
      1000      1010      1020      1030      1040      1050      1060

1330      1340      1350      1360      1370      1380      1390
Hum.  AATGAGTCAGCTCTCTGGACTGCACATATGATGGAAGAAAGCAAGCGAACAATGCTTCCGAAGATCAGATG
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::
WC1  --TGCTCAACCTACAGGCTCTGC-----GGC-----CTCAGAGGACA-GCGCCC-----CCTACTG
      1070      1080      1090      1100

```

Fig. 26Q-5

```

1400      1410      1420      1430      1440      1450      1460
Hum.  CTGGAGTAATTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGCTCATAGCCCTGTATGG
      :: ...      :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG--GACGGGG-GC--GGTCCCTGCGCCGG
1110      1120      1130      1140      1150      1160

1470      1480      1490      1500      1510      1520
Hum.  GAGATTGGAGGTGAAATACCAAGGAGAGTGGGGGACTGTGTGTCATGACAGATGGAGCACAAGG-AATGC
      :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  GAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC
1170      1180      1190      1200      1210      1220

1530      1540      1550      1560      1570      1580      1590
Hum.  A-GCTGTTGTGTAAACAATTGGGATGTGA-AAGCCTATGCAATGTTGGTATGACCTATTTAAAG
      :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG
1230      1240      1250      1260      1270      1280      1290

1600      1610      1620      1630      1640      1650      1660
Hum.  AAGCATCAGGACCCTATTGGCTGGATGACGTTTCTTGCAATTGGAAATGAGTCAAAATATCTGGGACTGTGA
      :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CAGGATCAGGGCCCATCTGGTTGGACAACCTTGAACCTGCACAGGAAAGAGTCCCACGTGTGGAGGTGCCC
1300      1310      1320      1330      1340      1350      1360

```

Fig. 26Q-6

Fig. 26Q-7

	1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCA	TGCAGGAACAGTGGTG--GGAAATAATGAC					
 : : : : : : : : : : : : : :						
WC1	-AGAATCCAGTGTGGAAAACTGACACCCTCTCT--CTGGCAGTGTCCCTCTGACCCCTTGGAATTACAAC						
	1640	1650	1660	1670	1680	1690	1700
	2020	2030	2040	2050	2060	2070	2080
Hum.	TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGGAGCTGAGGCTTGTGGG						
	: : : : . . : : : : : : : : : : : : : : : : : :						
WC1	T-CATGCTCTCCAAAGGAGGAAGCCCTATATCTGGTGTGCAGACAGCACACA--GATCCGC--CTGGTGGA						
	1710	1720	1730	1740	1750	1760	
	2090	2100	2110	2120	2130	2140	2150
Hum.	TGGAAGCAGCAGGTGTGCTGGAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCGTGTGCTAAT						
	: :						
WC1	TGGAGGTGGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGCAACCATCTGTGATGAC						
	1770	1780	1790	1800	1810	1820	1830
	2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCCAACCTTGAATGTGGGTCTGCAATCAGGGTCTCCA						
	: :						
WC1	CGCTGGGACCTGGACGATGCCCGTGTGGTGTGCAAGCAGCTGGCTGTGGAGAAGC---CCTGGACGCCCA						
	1840	1850	1860	1870	1880	1890	1900

Fig. 26Q-8

```

2230      2240      2250      2260      2270      2280
Hum.  GAGA-GCCTCATTTACAGAA--AGAACATTACACATCTTAATGTGGAATCTGGCTGCACTGGAGGGGA
      .:. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CTGTCTCTTCCTTCTTCGGGACGGGATCAGGGCCCATCTGGCTGGATGAAGTGAACCTGCAGAGGAGAGGA
1910      1920      1930      1940      1950      1960      1970

2290      2300      2310      2320      2330      2340      2350
Hum.  AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAACAG-ACTGCGGTGTCAATTAAATATGGAAGCAAG
      . : : : : : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GTCCCCAAGTATGGAGGTGCCCTTCCCTGGGGATGGCGGCAACAAC-TGCAATCATCAAGAAGATGCAGG
1980      1990      2000      2010      2020      2030      2040

2360      2370      2380      2390      2400      2410      2420
Hum.  TTTGATCTGCTCAGCCACACAGGCAGCCAGGCTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTTGAA
      . : : : : : : : : . . : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  AGTCATCTGCTCAGGATTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGAGTAGAA
2050      2060      2070      2080      2090      2100

2430      2440      2450      2460      2470      2480      2490
Hum.  GTGAAACATGCAGACACATGGCGGCTCTGTCTGTGATTCTGATTTCTCTCTTCATGCTGCCAATGT--GCT
      : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GTGCATTTCTGGAGAAGCCTGGACCCCAAGTGTCTGATGGAAACTTCACACTCCCCACTGCCCAAGTCACT
2110      2120      2130      2140      2150      2160      2170

```

Fig. 26Q-9

Figure 26Q-10

	2500	2510	2520	2530	2540	2550	2560
Hum.	GTCCAGAGAAATTA	ATTGTGGAGATGCC	ATATCTCTTCTGT	GGAGATCACTTT	TGAAAAGG	-AATGG	
	
WC1	GTGCAGAGC--TGG	GATGTGGCAAGGCT	GTGTCT-GTCCTGG	GACACATGCCAT	TCAGAGAGTCCG	GATGG	
	2180	2190	2200	2210	2220	2230	2240
	2570	2580	2590	2600	2610	2620	2630
Hum.	TCTAACTTGGCCGAA	AAAGTTCCAGTGTGA	AGGAGTGAAACTCA	CCCTTGCAATTATG	CCCCCATTTGTTCA		
	
WC1	CCAGGTCTGGGCTGA	AGATTTCAGGTGTGA	TGGGGGGAGCCTGA	GCTCTGGTCCTG	CCCCCAGAGTGCCC		
	2250	2260	2270	2280	2290	2300	2310
	2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGGAAGACACT	TGTATCCACAGCAG	AGAAGTTGGAGTTG	TCTGTCTCCGATAT	ACAGATGTCCGAC		
	
WC1	TGTCCAGGAGGCAC	ATGTCTCCACAGTGG	AGCTGCTCAGGTTG	TCTGTTCAGTGTAC	ACAGAAAGTCCAGC		
	2320	2330	2340	2350	2360	2370	2380
	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAAT	CC---CAGTGTGACG	GGCAAGTGGAGATCA	ACGTGCT-TGGACA	CTGGGGCTCAC		
	
WC1	TTATGAAAAACGGCA	CCCTCTCAATGTGAG	GGGCAGGTGGAGAT	-GAAGATCTCTGGAC	GATGGAGAGCGC		
	2390	2400	2410	2420	2430	2440	2450

Fig. 26Q-10

```

2780      2790      2800      2810      2820      2830      2840
Hum.  TGTGTGACACCCACTGGGACCCAGAAAGATGCCCGTGTCTATGCAGACAGCTCAGCTGTGGACTGCTCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TCTGTGCCCTCCCACTGGAGTCTGGCCAATGTTGTCTGTCTCAGCTCGGCTGTGGAGTCGCCCAT
      2460      2470      2480      2490      2500      2510      2520

2850      2860      2870      2880      2890      2900      2910
Hum.  CTCAACCACAGGAGGAAAAATATATTGGAGAAAGAAAGTGTTCGTGTGGGGACACAGGTTTCATTGCTTA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CTCCACCCCAAGAGGCCACACTTGGTGGAAGGAGGTGATCAGATCTCAACAGCCCAATTTCACTGCTCA
      2530      2540      2550      2560      2570      2580      2590

2920      2930      2940      2950      2960      2970      2980
Hum.  GGGAATGAGTCACCTTCTGGATAACTGTCAAATGACAGTCTTGGAGCACCTCCCTGTATCCATGGAATA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GGGCTGAGTCCTTCCTGTGGAGTTGTCTGTGACTGCCCTTGGTGGCCCTGACTGTTCCCATGGCAACA
      2600      2610      2620      2630      2640      2650      2660

2990      3000      3010      3020      3030      3040      3050
Hum.  CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTTTCCATGCCCTCGCAAATGTATCTGACCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CAGCCTCTGTGATCTGCTCAGGAAACCAACACCCAGGTGCTGCCCCAGTGCAACGACTTCCTGTCTCAACC
      2670      2680      2690      2700      2710      2720      2730

```

Fig. 26Q-11

	3060	3070	3080	3090	3100	3110	3120
Hum.	ATATTGCTGCAGTTC	CAGAGGCAGTGT	TGATCTGTAGAG	CAAAACGGCTCC	GCCTAGTGGAT		

WC1	TGCAGGCTCTCGGCCT	CAGAGGAGAGTTCT	CCCTACTGCTCAG	ACAGCAGGCAAGCT	CCGCCTGGTGGAC		
	2740	2750	2760	2770	2780	2790	2800
	3130	3140	3150	3160	3170	3180	3190
Hum.	GGGACAGCCGCTGTG	CCCCGAGAGTAGA	TCTATCACGACGGCT	TCTGGGGCACCATCT	GTGTGATGACG		

WC1	GGGGCGGTCCCTGCG	CGGAGAGTGGAGAT	CCTTGACCAAGGCTC	CTGGGGCACCATCT	GTGTGATGATG		
	2810	2820	2830	2840	2850	2860	2870
	3200	3210	3220	3230	3240	3250	3260
Hum.	GCTGGACCTGAGCGAT	GCCCACGTGGTGTG	TCAAAAGCTGGGCTGT	GGAGTGGCCTTCAAT	GCCACGGT		

WC1	ACTGGACCTGGACGAT	GCCCCGTGGTGTG	CAGGCAGCTGGGCTGT	GGAGAAGCCCTCAAT	GCCACGGG		
	2880	2890	2900	2910	2920	2930	2940
	3270	3280	3290	3300	3310	3320	3330
Hum.	CTCTGCTCACTTTGG	GAGGGGTCAAGGGCC	CACTCTGGCTGGATG	ACCTGAACCTGCAC	AGGAACGGAGTCC		

WC1	GTCTGCTCACTTCGG	GGCAGGATCAGGGCC	CACTCTGGCTGGACG	ACCTGAACCTGCAC	AGGAAGGAGTCC		
	2950	2960	2970	2980	2990	3000	3010

Fig. 26Q-12

```

3340 3350 3360 3370 3380 3390 3400
Hum. CACTTGTGCAGTGCCCTTCCCGCGGCTGGGGCAGCACGACTGCAGGCACAAGGAGGACGCGAGGGGTCA
    ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  CACGTGTGGAGGTGCCCTTCCCGGGGCTGGGGCGGCACGACTGCAGACACACAAGGAGGACGCCGGGGTCA
    3020 3030 3040 3050 3060 3070 3080

3410 3420 3430 3440 3450 3460 3470
Hum. TCTGCTCAGAAATTCACAGCCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGA
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  TCTGCTCAGAGTTCCCTGGCCCTCAGGAT----GGTGAG-CGAGGACCCAGCAG-TGTGCTGGGTGGCTGGA
    3090 3100 3110 3120 3130 3140

3480 3490 3500 3510 3520 3530 3540
Hum. AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACACAGCCATAGCAGGCATTGTG
    :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  GGTTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCGAGCCCCCATGGAAGATATCACTGTGTCCGTGATC
    3150 3160 3170 3180 3190 3200 3210

```

Fig. 26Q-13

Fig. 26Q-14

```

Hum.  -----TGC-----3750      3760
      ::::
WC1  TGTCCAACTGCTGCCGCTGCACACAGAGAGAACTCCGCCTCAGGGGAGGAGACAGCGAGTGCTCAG
3430 3440 3450 3460 3470 3480 3490

3770      3780      3790      3800      3810      3820      3830
Hum.  GGAGAGTGGAGATCTGGCACGCAGGCTCCTGGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCCGAGGC
:: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
WC1  GCGGGTGGAGGTGTGGCACAAACGGCTCCTGGGGCACCCGTGTGCGATGACTCCTGGAGCCTGGCAGAGGC
3500 3510 3520 3530 3540 3550 3560

3840      3850      3860      3870      3880      3890      3900
Hum.  GGAAGTGGTGTGTACAGCAGCTGGGCTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTGGCCAG
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
WC1  TGAGGTGGTGTGTACAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGTGCGGTCTGCAGCATTTGGCCCT
3570 3580 3590 3600 3610 3620 3630

```

Fig. 26Q-15

```

3910      3920      3930      3940      3950      3960      3970
Hum.  GGAAC TGGAA CCA TCTGG TTGAT GACAT GCGGT GCAA AAGAA ATGAG TCATT CTAT GGGAC TGTCA CG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GGAAT TGGAG CATCTGG CTGGA CAGAG GTGCA GTGCG GGGCC GGGAG TCCCT GTTGG GACTGTG GTTG
3640      3650      3660      3670      3680      3690      3700

3980      3990      4000      4010      4020      4030      4040
Hum.  CCAAA CCTT GGGAC AGAGT GACTG TGGAC ACAAG GAAAT GCTGG CGTG AGGTG CTTGG ---ACAGTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CGGAG CCCCT GGGGG CAGAG CGGAC TGCAA AGCAC GAGAG GATG CTGGT GTGAG GTGCT CTGGT GTAAG GAC
3710      3720      3730      3740      3750      3760      3770

4050      4060      4070      4080      4090
Hum.  G----- CTGAA AATCA CTTGAA TG-- CCT----- CCTC AGGT-CATT ---TAGCA -CTTA TTTAT CCA
      . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   AACATTG CCCCAC GACCA CAGCA GGGAC CAGAA CAACT CAAAT TCTCT CCCCT GGCAT CTCTC CCCTGC CT
3780      3790      3800      3810      3820      3830      3840

```

Fig. 26Q-16

```

Hum. 4100      4110      4120      4130      4140
G-----TATCTT----TGGGCTC-CTTCTC---CTGGTCT-----GTTTATTCTATTCTCA
:      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :
WC1  GGGTTCTCTGCCTTATCCTGGGGTCGCTTCTCTTCCCTGGTCCTCGTCATCCTGGTGACTCAGCTACTCA
3850      3860      3870      3880      3890      3900      3910

Hum. 4150      4160      4170      4180
CGTGGTG--CCGAGTTCAGAAACAAAAACATCT-----GCCC---CT----CAGAGTT-----
.:      :      :      :      :      :      :      :      :      :
.:      :      :      :      :      :      :      :      :      :
WC1  GATGGAGCAGAGCGCAGAGCCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT
3920      3930      3940      3950      3960      3970      3980

Hum. 4190      4200      4210      4220
-----CAAC-----CAGAAGGAGGG---GTTCT-CTCG---AGGAGAAATTATCCATGA-----
:      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :
WC1  CGATTACCTTCTGACACACAGAAGGAGGTCTGGGCAGCCCAGATCAGATGACTGATGTCCCTGATGAAAAAT
3990      4000      4010      4020      4030      4040      4050

```

Fig. 26Q-17

```

4230
Hum.  ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGGGAC
      :::::      :::::      :::::      :::::      :::::
WC1  TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACCTCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060  4070  4080  4090  4100  4110  4120

4260  4270  4280  4290
Hum.  CCACATGGGACAAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :::: ::::: ::::: ::::: ::::: :::::
WC1  CCCACAGAGAAGGAGGACGGGTGAGGTCCTCTCAGACAGGCTCTTCTGAACCTTCTCCAGAGAGGCAGC
4130  4140  4150  4160  4170  4180  4190

4300  4310  4320  4330
Hum.  ---CCATGGTT--GTGAAGA---TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . ::::: : ::::: ::::: .. ::::: . :::::
WC1  TAATCCTGGGGAAGGAGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGATGCTGGGTATGATGAT
4200  4210  4220  4230  4240  4250  4260

```

Fig. 26Q-18

4340

Hum. CTT-----CCTG-----CCTCTGAAGCCACAAAA

4350

WC1 GTTGAAC TCAGT G C C C C T G G G A A C A T C C C C A G T T T C T C G

4270 4280 4290 4300

Fig. 26Q-19

GTCGACCCACGCTCCGGTCTGTGGCTGAGC	M	A	L	P	A	L	G	L	D	P	W	S	12
	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	67
L L G L F L F L Q L L Q L L L P T T A G													32
CTC CTG GGC CTT TTC CTC TTC CAA CTG CTT CAG CTG CTG CCG ACG ACG ACC GCG GGG													127
G G G Q G P M P R V R Y Y A G D E R A													52
GGA GGC GGC CAG GGC CCC ATG CCC AGG GTC AGA TAC TAT GCA GGG GAT GAA CGT AGG GCA													187
L S F F H Q K G L Q D F D T L L L L S G D													72
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT													247
G N T L Y V G A R E A I L A L D I Q D P													92
GGA AAT ACT CTC TAC GTG GGG GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA													307
G V P R L K N M I P W P A S D R K K S E													112
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA													367
C A F K K K S N E T Q C F N F I R V L V													132
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT													427
S Y N V T H L Y T C G T F A F S P A C T													152
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC													487
F I E L Q D S Y L L P I S E D K V M E G													172
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA													547

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Fig. 27A

GenBank

K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607
L	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787
E	F	D	F	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847
V	G	G	E	K	L	L	Q	K	K	W	T	T	F	L	K	A	Q	L	L	292
GTG	GGC	GGC	GAA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	L	P	A	312
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	332
GAT	TCT	CCC	ACA	GCT	CCC	CAC	ATC	TAC	GCA	GTC	TTC	ACC	TCC	CAG	TGG	CAG	GTT	GGC	GGG	1027
T	R	S	S	A	V	C	A	F	S	L	L	D	I	E	R	V	F	K	G	352
ACC	AGG	AGC	TCT	GCG	GTT	TGT	GCC	TTC	TCT	CTC	TTG	GAC	ATT	GAA	CGT	GTC	TTT	AAG	GGG	1087

Fig. 27B

K Y K E L N K E T S R W T T Y R G P E T 372
 AAA TAC AAA GAG TTG AAC AAA GAA ACT TCA CGC TGG ACT ACT TAT TAT AGG GGC CCT GAG ACC 1147

 N P R P G S C S V G P S S D K A L T F M 392
 AAC CCC CGG CCA GGC AGT TGC TCA GTG GGC CCC TCC TCT GAT AAG GCC CTG ACC TTC ATG 1207

 K D H F L M D E Q V V G T P L L V K S G 412
 AAG GAC CAT TTC CTG ATG GAT GAG CAA GTG GTG GGC ACG CCC CTG CTG GTG AAA TCT GGC 1267

 V E Y T R L A V E T A Q G L D G H S H L 432
 GTG GAG TAT ACA CGG CTT GCA GTG GAG ACA GCC CAG GGC CTT GAT GGC CAC AGC CAT CTT 1327

 V M Y L G T T T G S L H K A V V S G D S 452
 GTC ATG TAC CTG GGA ACC ACC ACA GGG TCG CTC CAC AAG GCT GTG GTA AGT GGC GGC GAC AGC 1387

 S A H L V E E I Q L F P D P E P V R N L 472
 AGT GCT CAT CTG GTG GAA GAG ATT CAG CTG TTC CCT GAC CCT GAA CCT GTT CGC AAC CTG 1447

 Q L A P T Q G A V F V G F S G G V W R V 492
 CAG CTG GCC CCC ACC CAG GGT GCA GTG TTT GTA GGC TTC TCA GGA GGT GTC TGG AGG GTG 1507

 P R A N C S V Y E S C V D C V L A R D P 512
 CCC CGA GCC AAC TGT AGT GTC TAT GAG AGC TGT GTG GAC TGT GTC CTT GCC CGG GAC CCC 1567

 H C A W D P E S R T C C L L S A P N L N 532
 CAC TGT GCC TGG GAC CCT GAG TCC CGA ACC TGT TGC CTC CTG TCT GCC CCC AAC CTG AAC 1627

Fig. 27C

S W K Q D M E R G N P E W A C A S G P M 552
TCC TGG AAG CAG GAC ATG GAG CGG GGG AAC CCA GAG TGG GCA TGT GCC AGT GGC CCC ATG 1687

S R S L R P Q S R P Q I I K E V L A V P 572
AGC AGG AGC CTT CGG CCT CAG AGC CGC CCG CAA ATC ATT AAA GAA GTC CTG GCT GTC CCC 1747

N S I L L E L P C P H L S A L A S Y Y W S 592
AAC TCC ATC CTG GAG CTC CCC TGC CCC CAC CTG TCA GCC TTG GCC TCT TAT TAT TGG AGT 1807

H G P A A V P E A S S T V Y N G S L L L 612
CAT GGC CCA GCA GTC CCA GAA GCC TCT TCC ACT GTC TAC AAT GGC TCC CTC TTG CTG 1867

I V Q D G V G G L Y Q C W A T E N G F S 632
ATA GTG CAG GAT GGA GTT GGG GGT CTC TAC CAG TGC TGG GCA ACT GAG AAT GGC TTT TCA 1927

Y P V I S Y W V D S Q Q D Q T L A L D P E 652
TAC CCT GTG ATC TCC TAC TGG GTG GAC AGC CAG CAG GAC CAT CCG TTG ACC AGG GTC AGT GGT GGC GAA 1987

L A G I P R E H V K V P L T R V S G G A 672
CTG GCA GGC ATC CCC CGG GAG CAT GTG AAG GTC CCG TTG ACC AGG GTC AGT GGT GGC GGC 2047

A L A A Q Q S Y W P H F V T V T V L F A 692
GCC CTG GCT GCC CAG CAG TCC TAC TGG CCC CAC TTT GTC ACT GTC ACT GTC CTC TTT GCC 2107

L V L S G A L I I L V A S P L R A L R A 712
TTA GTG CTT TCA GGA GCC CTC ATC ATC CTC GTG GCC TCC CCA TTG AGA GCA CTC CGG GCT 2167

Fig. 27D

R	G	K	V	Q	G	C	E	T	L	R	P	G	E	K	A	P	L	S	R	732
CGG	GGC	AAG	GTT	CAG	GGC	TGT	GAG	ACC	CTG	CGC	CCT	GGG	GAG	AAG	GCC	CCG	TTA	AGC	AGA	2227
E	Q	H	L	Q	S	P	K	E	C	R	T	S	A	S	D	V	D	A	D	752
GAG	CAA	CAC	CTC	CAG	TCT	CCC	AAG	GAA	TGC	AGG	ACC	TCT	GCC	AGT	GAT	GTG	GAC	GCT	GAC	2287
N	N	C	L	G	T	E	V	A	*											762
AAC	AAC	TGC	CTA	GGC	ACT	GAG	GTA	GCT	TAA											2317
ACT	CTA	GGC	CAC	AGG	CGG	TGC	AGG	CAC	CTG	GGC	ATG	CTG	GGC	GGC	CCCA	AGC	CAC	AGC	CCCT	2396
TGAC	AGC	CAC	CAAA	AGAC	CACT	TTCT	CCCC	TGAG	AGG	AGCT	TTCT	GCT	ACT	CTG	CAT	CAC	TGAT	GAC	ACT	2475
TGAT	GAC	AGC	AGT	CTG	CCCT	ATG	GGAC	TCCCT	TTCT	ACCA	GCAC	ATG	AGT	CTCT	AAC	AGGT	GGGG	CTAC	CC	2554
CCAG	ACCT	GTCT	CTAC	ACT	GAT	ATT	GAAG	AAC	CTG	GAG	AGG	ATC	CTT	CAG	TTCT	GGCC	ATTC	CAG	GGAC	2633
CAC	AGT	TTCA	AGAT	CTA	AAAA	AACT	GCCT	GTCC	CAG	ACCT	ATG	GTAT	GAAC	ACCA	CAAC	ATCT	AAACA	ATC		2712
ATAT	GCTA	ACAT	GCC	ACT	CTG	AACT	CCACT	CTGA	AGCT	GCCG	TTTG	GAC	ACCA	CAC	ATC	CCCT	TTCT	CCAG	GGTCA	2791
TGC	AGG	ATCT	GTCT	CCCT	CCCT	TACC	AGTC	GTG	CAC	CGCT	GACT	CCC	AGGA	GTCT	TTCT	CTGA	AGT	CTG	ACC	2870
ACCT	TTCT	TTCT	TTG	CTT	CAG	TTGG	GCAG	ACT	CTG	ATCC	CTT	GTCC	CTGG	CAG	AAAT	GTG	AGC	CTT	CT	2949
TCAC	TCCT	TTAC	CCCT	AGCT	GTAC	CCCT	CTCC	CCCT	CTCC	CTT	TTCT	TTCT	TTG	GAT	TCAG	AAAT	CTG	CTT	CT	3028
AGAC	ACT	GT	TTAT	TTTT	TTAT	TAA	AAAT	ATA	AAG	CTT	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	3104

Fig. 27E

Fig. 27F

Hum.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQVGGTRSSAVCAFSLLDIERVF						
	::						
Mur.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQVGGTRSSAVCAFSLLDIERVF						
	::						
Hum.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFIMDEQVVGTPLLVKSGVEYTRLAV						
	::						
Mur.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFIMDEHVVGTPLLVKSGVEYTRLAV						
	::						
Hum.	430	440	450	460	470	480	490
	ETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGA VFGVSGGVW						
	::						
Mur.	430	440	450	460	470	480	490
	ESARGLDGSSHVVMYLGTSTGPLHKAVVPQDSSAYLVEEIQLSPDSEPVVRNLQLAPAQGA VFAFGSGGIW						
	::						
Hum.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCV LARDPHCAWDPE SRTCCLLSAPNLNSWKQDMERGNPEWACASGPM S RLPQS						
	::						
Mur.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCV LARDPHCAWDPE S RLC SLLSGST-KPWKQDMERGNPEWVCTRGPMARSPRRQS						
	::						

Fig. 27G

Figure 27H

Hum.	570	580	590	600	610	620	630
	RPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLVQDGVGGLYQCWATENG						

Mur.	560	570	580	590	600	610	620
	PPQLIKEVLTVPNSILELRCPHLSALASYWWSHGGRAKISEASATVYNGSLLLLLPQDGVGGLYQCVATENG						

Hum.	640	650	660	670	680	690	700
	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALI						

Mur.	630	640	650	660	670	680	690
	YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPFLIVTVLLAIVLLGVLT						

Hum.	710	720	730	740	750	760	
	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCILGTEVA						

Mur.	700	710	720	730	740	750	760
	LLLASPLGALRARGKVQGCGLPPREKAPLSRDQHLQPSKDHRTSASDVDADNHHLGAEVA						

Fig. 27H

```

Hum.  GTCG-AC-CC-----ACG-----CGTCCGGT-----CTGTGGCTGAGCATGGC
      :: :: ::
Mur.  CTCGGACGCCTGGGTTAGGGTCTGTACTGCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC
      10  20  30  40  50  60  70

Hum.  CCTCCAGCCCTGGCCCTGGACCCCTGGAGCCTCCTGGGCCCTTTCTCTTCCAACCTGCTTC-AGCTGCT
      40  50  60  70  80  90  100
Mur.  CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTCTTTCTTCCAACCT-CTTCCTGCTGCC
      80  90  100  110  120  130

Hum.  GCTGCCGACGACACCGCGGGGGGAGGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGAT
      110  120  130  140  150  160  170
Mur.  ATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGAC
      140  150  160  170  180  190  200

Hum.  GAACGTAGGGCACTTAGCTTCTTCCACCAAGAGGCCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTG
      180  190  200  210  220  230  240
Mur.  GGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGCCCTCCGAGACTTTGACACGCTGCTCCTGAGTGACG
      210  220  230  240  250  260  270

```

Fig. 27I

Fig. 27J

	530	540	550	560	570	580	590
Hum.	GGAGACAAGGTCAATGGAGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTT						

Mur.	GATAGACAAGGTCAATGGACGGGAAGGGCCAAAGCCC-TTTGACCCCTGTTCAACAAGCACACAAGCTGTCTT						
	560	570	580	590	600	610	620
	600	610	620	630	640	650	660
Hum.	GGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACA						
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAACCTTCCTGGGCAGCGAGCCCATCCTGATGCGGACACA						
	630	640	650	660	670	680	690
	670	680	690	700	710	720	730
Hum.	CTGGGATCCCAGCCTGTCCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGG						

Mur.	CTGGGATCCCATCCTGTTCCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGATGCCCTCCTTCGTGG						
	700	710	720	730	740	750	760
	740	750	760	770	780	790	800
Hum.	CAGCCATCCCCTTCGACCCAGGTCGTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA						

Mur.	CAGCCATCCCATCCACCCAGGTCGTCTATTCTTCTTCTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA						
	770	780	790	800	810	820	830

Fig. 27K

Fig. 27L

```

1090      1100      1110      1120      1130      1140      1150
Hum.  GGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGGAGTACAAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACCTTACCGGGGCTCAGAGGTCAGCCCCGA
1120      1130      1140      1150      1160      1170      1180

1160      1170      1180      1190      1200      1210      1220
Hum.  GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTCCTGAT
1190      1200      1210      1220      1230      1240      1250

1230      1240      1250      1260      1270      1280      1290
Hum.  GGATAGCAAGTGGTGGGACGCCCTGCTGTTGTAATCTGGCGTGGAGTATACACGGCTTGCAAGTGGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGATAGCACGTGGTAGGAACACCCCTGCTGTTGTAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAG
1260      1270      1280      1290      1300      1310      1320

1300      1310      1320      1330      1340      1350      1360
Hum.  ACAGCCCAGGGCCTTGATGGGCACAGCCCATCTTGTGATGTACCTGGGAACCAACACAGGGTCGCTCCACA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TCAGCTCGGGCCCTTGATGGGAGCAGCCCATGTGGTCATGTATCTGGGTACCTCCACGGGTCCCTGCACA
1330      1340      1350      1360      1370      1380      1390

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Fig. 27M

```

1370      1380      1390      1400      1410      1420      1430
Hum.  AGGCTGTGTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCCCTGAACC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AGGCTGTGTCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTTCAGCTGAGCCCTGACTCTGAGCC
1400      1410      1420      1430      1440      1450      1460

1440      1450      1460      1470      1480      1490      1500
Hum.  TGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGCTGGAGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TGTTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTGGAGA
1470      1480      1490      1500      1510      1520      1530

1510      1520      1530      1540      1550      1560      1570
Hum.  GTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCCGGGACCCCACTGTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GTTCCCAGGGCCAAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGGACCCCTCACTGTG
1540      1550      1560      1570      1580      1590      1600

1580      1590      1600      1610      1620      1630      1640
Hum.  CCTGGGACCCCTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCCCCAACCTGAACCTCCTGGAAGCAGGACAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CCTGGGACCCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAAGCAGGACAT
1610      1620      1630      1640      1650      1660      1670

```

Fig. 27N

```

1650      1660      1670      1680      1690      1700      1710
Hum.  GGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGAACGCGGCAACCCGGAGTGGGTATGCACCCGTGGCCCCCATGGCCAGGAGCCCCCGGCTCAGAGCCCC
1680      1690      1700      1710      1720      1730      1740

1720      1730      1740      1750      1760      1770      1780
Hum.  CCGCAAAATCATTAAGAGTCCTGGCTGTCCCAACTCCATCCTGGAGCTCCCTGCCCCACCTGTCTCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CCTCAACTAATTAAAGAAAGTCCTGACAGTCCCAACTCCATCCTGGAGCTGCGCTGCCCCACCTGTCTCAG
1750      1760      1770      1780      1790      1800      1810

1790      1800      1810      1820      1830      1840      1850
Hum.  CCTTGGCCCTCTTATTGGAGTCATGGCCCCAGCAGCAGTCCCAGAGCCCTCTTCCACTGTCTACAAATGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CACTGGCCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGTACCGTCTACAAATGG
1820      1830      1840      1850      1860      1870      1880

1860      1870      1880      1890      1900      1910      1920
Hum.  CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGTCTCTACCACTGTGGGCAACTGAGAATGGCTTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CTCCCTCTTGCTGCTGCCGAGGATGGTGTCTGGGGCCCTCTACCACTGTGTGGCGACTGAGAACGGCTAC
1890      1900      1910      1920      1930      1940      1950

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Fig. 270

Fig. 27P

	2210	2220	2230	2240	2250	2260	2270
Hum.	GGGAGAGGCCCGTTAAGCAGAGACAACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA						

Mur.	GGGAAAAGGCTCCACTGAGCAGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA						
	2240	2250	2260	2270	2280	2290	2300
	2280	2290	2300	2310	2320	2330	2340
Hum.	TGTGGACGCTGACAACTGCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGG-CGGGGGCTG--C						

Mur.	CGTAGATGCCGACAAACCAATCTGGCGCCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC						
	2310	2320	2330	2340	2350	2360	2370
	2350	2360	2370	2380	2390	2400	2410
Hum.	GGTGAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCCTGACTAGGATGACAGCAGCACAAA						

Mur.	AGAGCAAGCCACTGGCCCTTGTTGGCTATGC---CAGGCACAG-----TGCCACTCT--						
	2380	2390	2400	2410			2420
	2420	2430	2440	2450	2460	2470	2480
Hum.	AGACCACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC						

Mur.	-GACCA-----GGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTCAC-CTACAG-----C						
		2430		2440	2450	2460	

Fig. 27Q

Fig. 27R

Figure 27S

```

                2760      2770      2780      2790      2800      2810
Hum.  ----GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AGCAGCTGCTGCTTTGAACACACAGCCACCCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT
        2730      2740      2750      2760      2770      2780      2790

                2820      2830      2840      2850      2860      2870      2880
Hum.  TTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTCTTCTGAAGTCTGACCACTTCTTCTTGTG
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TTCCCTTACCAGTCGGGCCATACCTGTTT---GGGAAGTCATCTCTGAAGTCTAACCACTTCTTCTTGG
        2800      2810      2820      2830      2840      2850

                2890      2900      2910      2920      2930      2940      2950
Hum.  TTCAGTTGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAAATGGCAGGGGTAATCTGAGCCTTCTTC
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCCTGGCTAGAAATGGGGGCATAATCTGAGCCTTGTTC
        2860      2870      2880      2890      2900      2910      2920

                2960      2970      2980      2990      3000      3010
Hum.  ACTCCCTTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCTCCCTTTTCTTGTTTGGGATTCAGA
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  ---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC---TCCCTTTGTTTGGGATTCAGA
        2930      2940      2950      2960      2970      2980      2990

```

Fig. 27S

```

3020      3030      3040      3050      3060      3070      3080
Hum.  AAAC TGCTGTCAGAGACTGTTATTTTATTTTATTTAAATAATAAGGCTTAAAAAATAAAAAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AAAC TGCTGTCAGAGACAATTTATTTTATTTTATTTTATTTAAAAA-----AGATATAA
      3000      3010      3020
3090      3100
Hum.  AAAAAAAGGCGGCCGC
      . . . . .
Mur.  GCTTTAAAG-----
      3040

```

Fig. 27T

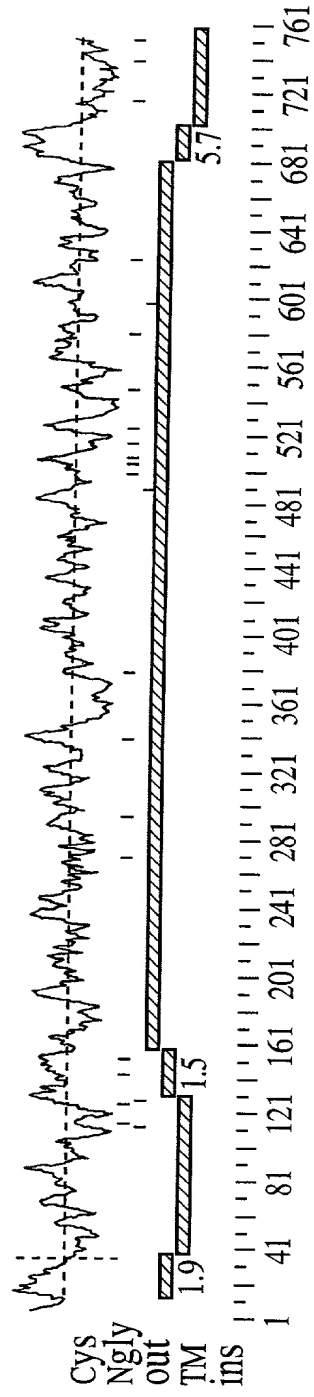


Fig. 27U

GTGACCCACGGTCCGCAGCTTTGGACACTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA	79
TCAAGAAAGGCCAGCACAGCAGAAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC	150
M C T K T I	
P V L W G C F L L W N L Y V S S Q T I	26
CCA GTC CTC TGG GGA TGT TTC CTC CTG TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT	210
Y P G I K A R I T Q R A L D Y G V Q A G	46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GGT CAA GCT GGA	270
M K M I E Q M L K E K K L P D L S G S E	66
ATG AAG ATG ATT GAG CAA ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG	330
S L E F L K V D Y V N Y N F S N I K I S	86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT	390
A F S F P N T S L A F V P G V G I K A L	106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA	450
T N H G T A N I S T D W G F E S P L F V	126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT	510
L Y N S F A E P M E K P I L K N L N E M	146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG	570

Fig. 28A

L C P I I A S E V K A L N A N L S T L E 166
 CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG 630

 V L T K I D N Y T L L D Y S L I S S P E 186
 GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA 690

 I T E N Y L D L N L K G V F Y P L E N L 206
 ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC 750

 T D P P F S P V P F V L P E R S N S M L 226
 ACC GAC CCC CCC TTC TCA CCA CCA GTT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC 810

 Y I G I A E Y F F K S A S F A H F T A G 246
 TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG 870

 V F N L T L S T E I S N H F V Q N S Q 266
 GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA 930

 G L G N V L S R I A E I Y I L S Q P F M 286
 GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG 990

 V R I M A T E P P I I N L Q P G N F T L 306
 GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG 1050

 D I P A S I M L T Q P K N S T V E T I 326
 GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC 1110

340/361

Fig. 28B

Figure 28C

V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	GTT	GGC	CTG	GTT	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	L	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTC	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	K	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500
TTGCCGGTTTGCAATTACCCAGGAAGTAAATGGTCCTTAATCCTACAACACTGTAAACCCAGAAAGGAAAGACAGT	1579																			
ACACACTGGAATTGTAAAGCCCTTGTTGAATTGCTTAGGCAGAAAGTTTCTTTCTTAAGCCTTCAGGAACCCAGAAATAA	1658																			
GGCAGACTCTGTTAAAGGGATAAATAGAGGTGCTGAATGTGAGTGTATGCATGCTGCCGTGTCTGTGTTTATGTTTG	1737																			
TTTGTTTGTGGGGCAAGAAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAGCAACTCTAAG	1816																			

Fig. 28C

TCTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCTACCTGCATATTGGTTTC 1895
ATGTTTATATTCACCTGTTACTATCTTCTGTGTTTAAATTTCTATCAAAAAAAAAAAAAAAAAAGGGC 1974
GGCCGC 1980

Fig. 28D

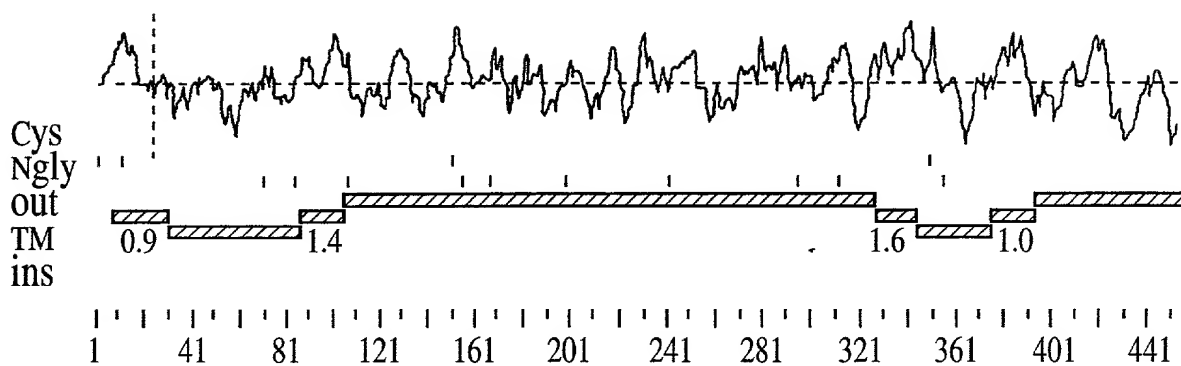


Fig. 28E

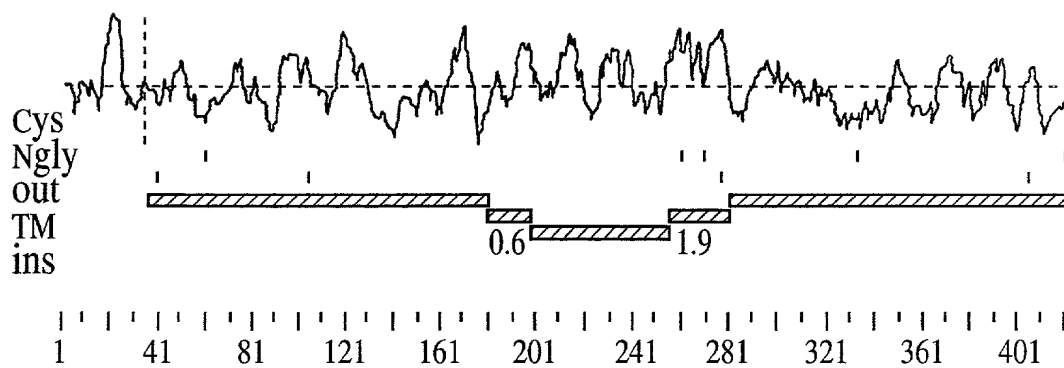


Fig. 29F

```

10      20      30      40      50      60
286 MCTKT-IPVLWGCFL-LWNLVSSSQTIYPGIKARITQRALDYGVAQGMKMIQMLKEKLPDLGSESL
      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
      10      20      30      40      50      60

      70      80      90      100     110     120     130
286 EFLKVDYVYNFNSNIKISAFSPNTSLAFVPGVGIGIKALTNHGTANISTDWGFESPLFVLYNSFAEPM--
      .      .      .      :      :      :      :      :      :      :
BPI KIKHLGKGHYSFYMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
      70      80      90      100     110     120     130

286 -----KPI-----140      150
      :      :
BPI SISADLKLGSNPITSGKPTITCSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
      140     150     160     170     180     190     200

      160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDLNLKGVFYPLENLTDPFSPVPFVLPERSN
      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLPVMTKIDSVAGINYGVLVAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAMD
      210     220     230     240     250     260     270

```

Fig. 28F

Fig. 28G

```

10      20      30      40      50      60
286 MCTKTIPVLWGCFLWNLYVSSSQTI--YPGIKARITQRALDYGVDQAGMKMIEQMLKEKKLPDLSGSESL
: . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP MGALARAL--PSILLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIGKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
RENP RIPHVGRGRYEFHSLNIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----LKN-LNEMLCPIIASE
: :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
RENP SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFSPVPFVLPERSN
: . :. . :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
RENP VSSKLQPYFQTLVPVMTKIDSVAGINYGVLVAPPATTAEITLDVQMKGEFYSENHHNPPPFAPPVMEFPAHD
210     220     230     240     250     260     270

```

Fig. 28H

```

230      240      250      260      270      280      290
286 SMLYIGIAEYFFKSASFHFTAGVFNLTSTEEISNH--FVQNSQGLGNVLSRIAEIFYILSQPFMVRIMA
      :::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
RENP RMVYLGSLSDYFFNTAGLVYQEAAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFP-NMKIQIHVSA
      280      290      300      310      320      330      340

      300      310      320      330      340      350      360
286 TEPPINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTVGLVILGQRLVCSLSLNRFRLLALPE
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP STPPHLSVQPTGLTFYPADVQALAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKH
      350      360      370      380      390      400      410

      370      380      390      400      410      420      430
286 SNRSNIEVLRFFENILSSILHFGVLPANAKLQQGFPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK
      :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP SNIGPFPVELLDIMNYIVPILVLRVNEKLGKGFPLPTPARVQLYNVVLQPHQNFLFGADVVK-----
      420      430      440      450      460      470      480

      440      450
286 QQPSFHVWEGNLNLSRQWRGKSAP

RENP -----

```

Fig. 28I

GTCGACCCACGCGTCCGGGGAATTGCAGCAGGAAAAATATGTGAAGAGTTTTTAAACCCACAAAATTCTTCTTACTTTAGA 79
 ATTAGTTGTACATTGGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG 8
 W I V S H R M E M W L L I L V A Y M F Q 28
 TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG 209
 R N V N S V H M P T K A V D P E A F M N 48
 AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT 269
 I S E I I Q H Q G Y P C E E Y E V A T E 68
 ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA 329
 D G Y I L S V N R I P R G L V Q P K K T 88
 GAT GGG TAT ATC CTT TCT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA 389
 G S R P V V L L Q H G L V G G A S N W I 108
 GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT 449
 S N L P N N S L G F I L A D A G F D V W 128
 TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG 509
 M G N S R G N A W S R K H K T L S I D Q 148
 ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA 569

Fig. 29A

D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I	168
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA	629
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G	188
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC	689
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M	208
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG	749
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F	228
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT	809
L	L	L	P	D	M	M	I	K	G	L	F	G	K	K	E	F	L	Y	Q	248
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG	869
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I	268
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT	929
C	S	N	I	M	L	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA	989
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W	308
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG	1049
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N	328
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT	1109

Fig. 29B

L E K C N Q CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT P 348
CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT 1169

T A M W T G G Q D W L S N P E D V K M L 368
ACA GCA ATG TGG ACA GGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG 1229

L S E V T N L I Y H K N I P E W A H V D 388
CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT 1289

F I W G L D A P H R M Y N E I I H L M Q 408
TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG 1349

Q E E T N L S Q G R C E A V L * 424
CAG GAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA 1397

AGCATCTGACACTGACGATCTTAGGACAAACCTCCTGAGGGATGGGGCTAGGACCCATGAAGGCAGAAATTACGGAGAGCA 1476
GAGACCTAGTATACATTTTTCAGATTCCTGCACTTGGCAGTAAATCCGACACTTACATTTTCTGTAAA 1555
TTAAAGTACTTATTAGGTAAATAGAGGTTTGTATGCTATTATATATTCTACCATCTTGAAGGGTAGGTTTACCTGAT 1634
AGCCAGAAAATATCTAGACATTCTCTATATCATTGAGGTTTCTTAAACACCTATTGTTTCTCTATAAGCCAT 1713
ATTTTGGAGCCTAAAGTAAATGGCAAAATGGGACAGATAATTGAGGCTCTGAGTCTGTGATATTGTTGACTTTGA 1792
CAAAATAAGCTAGACATTTTACCTTGTGCCCACAGAGACATAACACTACCTCAGGAAGCTGAGCTGCTTAAAGGACAA 1871
CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATCTCAGAAATAAGGCCAAGTTTATAGTTGCA 1950
TCTCAGGGGAGAAAATTTTATAGGATGTTTATGAGTCTCTCCAATAAATGCATTTCTGCATTACATAAAAAA 2029
AAAAAGGGCGCGC 2044

Fig. 29C

```

10      20      30      40      50      60      70
294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIHQHGYPCEEYEVATEDG
:   ...   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP M-----WLL---LTMASLISVLGTTGHLFGKLH-----PGSPEVTMNIQMITYWGYPNEEYEVVTEDEG
10      20      30      40      50

80      90      100     110     120     130     140
294 YILSVNRIPRGLVQPKKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNWSRK
:   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP YILEVNRIPYGKKNSGNTGQRPVVFLQHGLLASATNWNISNLPNNSLAFILADAGYDVWLGNRCNTWARR
60      70      80      90      100     110     120

150     160     170     180     190     200     210
294 HKTLSIDQDEFWAFSYDEMAREFDLPAVINFILQKTGQEKIYYVGYSGTTMGFIAFSTMPPELAQIKMYF
.   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQKQLHYVGHSGTTIGFIAFSTNPSLAKRIKTFY
130     140     150     160     170     180     190

220     230     240     250     260     270
294 ALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDDQICSNIMLLLGFF
:   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP ALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF
200     210     220     230     240     250     260

```

Fig. 29D

```

280      290      300      310      320      330      340
294 NTNNMMSRASVYAAHTLAGTSVQNIHLWSQAVNSGELRAFDWGSETKNLEKCNQPTPVR YRV RDMTVPT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP DSKNFNTSRLLDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVVTAMNVPI
      270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 AMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGRC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP AVWNGGKDLLADPQDVGLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----
      340      350      360      370      380      390

420
294 EAVL

HLP ----

```

Fig. 29E

```

10      20      30      40      50      60
294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTK--AVDPEAFMNISEIIHQHGYPCEEYEVATE
:      :...: . . . . :      :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCLVLWPLHSEGGKLTAVDPETNMNVSEIISYWGFPSSEYLVETE
      10      20      30      40      50

70      80      90      100     110     120     130
294 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGASNWISNLPNNSLGFILADAGFDVWMGNSRGNAWS
:      :      : .      :      :      :      :      :      :      :
LAL DGYILCLNRI PHGRKNHSDKGPVVF LQHGLLADSSNWVVTNLANSSLGFILADAGFDVWMGNSRGNTWS
      60      70      80      90      100     110     120

140     150     160     170     180     190     200
294 RKHKTLSDQDEFWAFSYDEMAREFDLPVINFILQKTGQEKIYYVGYSQGTMTMGFIASFSTMPELAQKIKM
:      :      :      :      :      :      :      :      :      :      :
LAL RKHKTLVSQDEFWAFSYDEMAYDLPASINFILNKTGQEQVYVVGHSQGTIGFIASFQIPELAKRIKM
      130     140     150     160     170     180     190

210     220     230     240     250     260     270
294 YFALAPIATVKHAKSPGTFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLGG
:      :      : . . . . :      :      :      :      :      :      :
LAL FFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKFELPQSAFLKWLGHVTHVILKELCGNLCFLLCG
      200     210     220     230     240     250     260

```

Fig. 29G

Figure 29H

```
280      290      300      310      320      330      340
294 FNTNNMMSRASVYAAHTLAGTSVQNIILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRVVRDMTVP
   :: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNNMLHWSQAVKFKQAFDQWSSAKNYFHYNQSYPPTYNVKDMMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: .
LAL TAVWSGGHDWLADVVDVNILLTQITNLVFHESIPWEHLDFIWGLDAPWRLYNKIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----
```

Fig. 29H

		M		S		2	
GTCGACCCACGGCTCCACGGCAGGGCTCCCGGGCGCAGCATTGCCCCCTGCACCACCTCACCAAG ATG GCT						75	
T L G H T F P F Y A G P K P T F P M D T							22
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC							135
T L A S I I M I F L T A L A T F I V I L							42
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG							195
P G I R G K T R L F W L L R V V T S L F							62
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC							255
I G A A I L A V N F S S E W S V G Q V S							82
ATC GGG GCT GCA ATC CTG GCT GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC							315
T N T S Y K A F S S E W I S A D I G L Q							102
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG							375
V G L G G V N I T L T G T P V Q Q L N E							122
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG							435
T I N Y N E E F T W R L G E N Y A E E C							142
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT							495
A K A A L E K G L P D P V L Y L A E K F T							162
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT							555

Fig. 30A

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

Fig. 30B

L * 344
TTA TAA 1101

CATTCTCCCGTGGAGGCCACCTGGACTTCAGTCTGGCTCCAAACCTCAATTGGCGCCCATATAAACCCAGCAGAACTG 1180
CCCTCAGGGTGGCTGTACCAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT 1259
AAAAAACAAAAACAAAAAGCCCTAAGGACTGAAGAGATGCTGGGCTGTCCATAAAGCCCTGTGCCATGATAAG 1338
GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCTTCCGTGCTGCCCTTCAAGATGCTATTCACCTGA 1417
AACCTAACTTCACCCCATAAACACAGCAGGGTGGGGTTACATATGATTCTCCCTATGGTTTCCCTCTCATCCCTCGGCA 1496
CCTCTGTTTTCCTTTCCTGGTTCCTTTTGTCTTCCTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA 1575
AGACAGCACTGGAAAGGAGGGGAAACCAAACCTTCTCATCCTAGGTCTAACATTAAACCACTATGCCACATTCCTCTTGA 1654
GCTTCAGTCCCAAATTTGCTACATAAGATTGCAAGACTTGCCAAAGATCTTGGGATTTATCTTCTATGCCCTTGCTGA 1733
CACCTACCTTGGCCCTCAAACACACACCTCACAAAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAACGCTATTCCT 1812
TCCCACCCCACTCAGCTGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGTGACCTGCCCTCATCACTGCCACCTAA 1891
CGTCCCTTGGGTGGTTCAGAAAGATGCTAGCTCTGGTAGGTCCTCCGGCCTCACTAGAGGGCGCCCTATTACTC 1970
TGGAGTCGACGCAGAGAAATCAGGTTTCACAGCACTGCGGAGAGTGTAAGCTGTCTCCAGCCAGCGAAAGCTCATGA 2049
GGACGTGCGACCCCGCGGAGAGCCATGAAAATTAATGGGAAAAAACAGTTTAAAAAAGGGCG 2128
GCGGC 2133

Fig. 30C

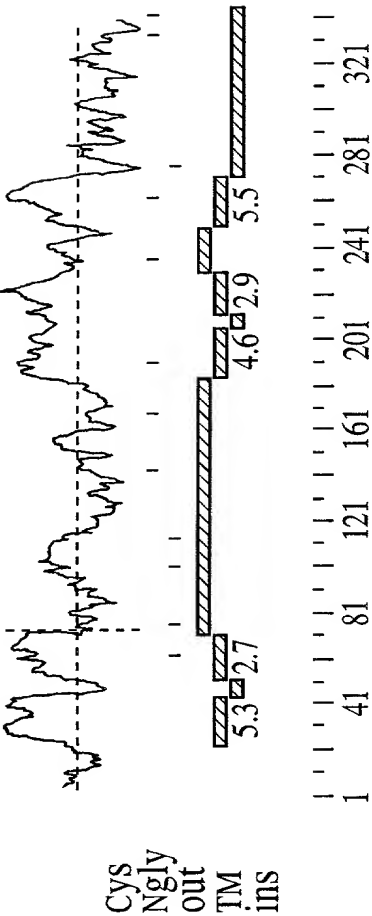


Fig. 300

```

10      20      30      40      50      60      70
296 MATLGHFFPYAGPKPTFPMDTTLASIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLSFIGAAILAV
: .. :... .. :... .. :... .. :... .. :... .. :... .. :... ..
CRP M-RIAH-----ASSRGNI-----SIFSFLIPLIAYILILPGVR-RKRVVTTVTYVLMMLAVGGALIAS
10      20      30      40      50
296 NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGGVNITL-----TGTPVQQQLNETIN--YNEEFTW
. . . : . :... :... :... :... :... :... :... :... :... :
CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTLLKFERLLSSNDVLPGSDMTELYYNEGFDI
60      70      80      90      100      110      120      130

```

Fig. 30E

```

140      150      160      170      180      190      200
296 RLGENYAECAKALEKGLPDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLSM
    . : : . : : : : : : : : : : : : : : : : : : : : : : : : :
CRP SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCISVVLMFL
    130      140      150      160      170      180      190

210      220      230      240      250      260
296 PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLHTHHGPAF---WITLTGLLCVL
    : : . : : : : : : : : : : : : : : : : : : : : : : : : :
CRP PHNAYKS--ILATGISCLIACLVYL---LLSPCELRIAFGTGENFERVDLTATFSFCFYLIFAIGILCVL
    200      210      220      230      240      250      260

```

Fig. 30F

Cell "Cell"

```

270      280      290      300      310      320
296 LGLAMAVAHRMQPHRLKAFNQSVDEDPMLEW-----SPEEGLLSPRY--RSMADSPKSQDIPLSEAS
CRP  CGGLGICEHWRIYTLSTFLDASLDEHVGPWKKLPTGGPALQGVQIGAYGTNTTNSSRDKNDISSDKTA
      270      280      290      300      310      320      330
      330
296 STKAY-----CK-----EAHPKDPD-----CA---L
CRP  GSSGFQSRSTSTCQSSASSASLRSQSSIETVHDEAELEERTHVHFLQEPCCSSST
      340      350      360      370      380

```

Fig. 30G